

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGCCAAGCC	CCTGCTGATG	CCCGAGCTGC	GCGAATGCGT	CACCGAGGGG	ACCGTCATTG		60
GTTCGCTGAA	GAAGATCGGG	GATTCTTTTC	AGGTTGACCA	CCCACTGCGT	GAGGTGTCGA		120
CCGACAAAGGT	GGCACCCGAG	ATCCGCTGC	CCTGCGCTGC	CCTCTTGTC	AGTATCGCC		180
CCCGACGAGA	CCGAGGCGTC	CCGTCGCGG	CCGAGCTGCT	CTGCGCTGCCG	AGATCGGCCG		240
AGATCGGCCG	CCGGCGCTCC	CCGACAGCCC	C				271

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala	Lys	Pro	Val	Ileu	Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly
1					5					10				15	
Thr	Val	Ile	Arg	Tyr	Leu	Lys	Ile	Gly	Asp	Ser	Val	Gln	Val	Asp	
									20		25		30		
Glu	Pro	Leu	Val	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro
								35		40		45			50
Ser	Pro	Val	Ile	Gly	Val	Leu	Val	Ser	Ile	Ser	Ile	Asp	Glu	Asp	Ile
								55		60		65			70
Thr	Val	Pro	Val	Gly	Glu	Leu	Ile	Arg	Ile	Gly	Val	Ile	Ile	Glu	
								75		75		80			85
Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro							
								85							

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAGCTTACCGG	ATGCGCTGGAG	GGGCACCCCA	GGACCGCGCC	GGAAACGGGG	GGGCGGGTCA		60
TTCGATATGTG	GGCGACGTTTC	GGTCCGTCG	GGAGGGCAT	TGACCGAT			107

(2) INFORMATION FOR SEQ ID NO:240:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAACTTCA	ATTTTGCTTC	CCTGAGTACT	CCCATCTCTG	CTTGTGCGAC	GGCGCTTGTG		60
TTTCCTGCCT	CGCTTGCAG	CGCAGATCCA	CCTGACCCGC	ATCGACCGGA	CATGACGAAA		120
GGCTATTGCC	CGCTGTGCGG	ATTCGGGTTT	GGCGACCTTG	CCCTGCGGA	CGCGGAGAAG		180
TACCCGACG	CGCTGTTTC	CGAACCTTG	ATCGAACCT	GTTTACCGG	CCCACAGTTT		240
TACTTCGATT	GTGCGAGCG	CGCTGACCGG	CTCGGCGGC	GGCGCGCACG	GGCTGGTTGC		300
CGCTGGCGAA	TTCCGTCGGA	CGACCCGAC	CGCTCGCTGA				339

(2) INFORMATION FOR SEQ ID NO:241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala							
1	5	10	15	20	25	30	35
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp							
36	40	45	50	55	60	65	70
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp							
75	80	85	90	95	100	105	110
Gly Phe Gly Asp Leu Ala Val Cys Asp GLY Glu Lys Tyr Pro Asp GLy							
96	101	106	111	116	121	126	131
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe							
136	140	145	150	155	160	165	170
Tyr Phe Asp Cys Val Ser Gly GLY Glu Pro Leu Pro Gly Pro Pro Pro							
175	180	185	190	195	200	205	210
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro							
215	220	225	230	235	240	245	250

(2) INFORMATION FOR SEQ ID NO:242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GTGACCAACGG TGGGCGTGC ACCAACCCCG GAGGGGAGC CGGGGGGGGCG CGGGGGGGCT	50
CGGGGGCGRA CGGGGGCGCG CGGGGGTACCG CGGGGGCGTC AGGGGGCGAG CGGGGGGGCG	130
GGGGGGATGG CGGGGGATGG AGCTTGGGGG CTACCGGGG CGGGGGGGCG ATGGGGGGCA	180
CGGGGGGGCG CGGGGGCGAG CGGGGGGGCG CGGGGGGGCG TGGGGGGAG CGGGGGGGCG	240
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	300
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	360
CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	371

## (2) INFORMATION FOR SEQ ID NO:243:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CTCCCCCTTC CACCAACCG CGGGGGGGCG CCTACCGGGCG GGGGGGCGCA CGGGGGGGTC	60
TTGACTCTTT CAACAAAGG CGCTTCTGTT TGGTTCGCA TGTGGGGCATG ATGTTGACCC	120
ATGGGGCAACG TGGACGTCGA CGATGGGGAC AAGGTTGAGG TCCATGGAA TGGGGGGCGC	180
CGTGGTGGAGC ATGGGGCTAG CGTGATAGC AGGGGGGGCG GTACCTGTTG CGGAGGCGCA	240
CGGGGGGGCG CGGGGGGGCG TGTGCTAGC GTGGGGGGCG AGGGGGGGCG TGGGGGGCGAT	300
CGTGGGGGGCG CGGGGGGGCG CGGGGGGGCG GTGGGGGGCG AGGGGGGGCG CGGGGGGGCG	360
CGGAGCTACCG CGGGGGGGCG AGGGGGGGCG CGGGGGGGCG CGGGGGGGCG CGGGGGGGCG	420
CGAC	424

## (2) INFORMATION FOR SEQ ID NO:244:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CGGGGGGGGG CGGGGGGGTG CACCGGATCG CGGGGGGGGG GTGGGAACGGT TTGGGGGGCG CGGGGGGGCT	60
TTGGGGGGCG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	120
AGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	180
TGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	240
GTGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	300
CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	317

## (2) INFORMATION FOR SEQ ID NO:245:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGCGTATGC	CGTTGCCGCG	TCAACGCCCT	GAGGCGATC	GTTTGCTTC	60
CGAGGAATG	TTCCGATCAG	ATCGCAGTGT	CCCTTGCTSC	ACCCACACCG	120
TGAACGTAGG	GGCGAAATTC	GGCGGAAATC	TGCGCTCTAG	TTCACGCTCG	180
GTTCCTGGAG	TTGGGTTGCCG	CTTTCTCGCG	GAACGGCGCG	GGCGCTCTCT	240
GGACAGGAG	ACCTTGATGC	CTATCTGCGT	CTCGATCTTC	ACCGCTCTCT	300
GCACCGCTC	TGGCGATGG	ACCCGAGAT	GGCGCTCGCG	GGCGACGCTC	360
GATGGCTCG	GGAGTTCTA	GAACCTGGT	CAACCGCTCG	GGCGCGCGA	420
AT					433

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDENESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

CGCTGGCGCT	GAACACCGAG	CGGGCGCTGC	CAGCTTCCC	GAACTCGCTA	GTGGCGCGGG	60
TGGCGTGT	CTCTCTCTGA	CGGGCGCG	CGACCGTAAG	GTGCGCTAATG	CCAGGGTAGC	120
GGCGGAGGTC	CATGAGCTCG	ATTCAGATGTC	GACTCTTCAG	CTCGCCGCC	GGGAGCTTGG	180
CATCGGGCT	GATCGGCCAG	GAACGGTAGG	ACAAAGCTGT	CGAAATCGATA	GTGGCTCGA	240
GAACGCGCT	GGCGCTTCCG	GGCGCTCTGA	GGCGGAAATG	CTTGATTTCT	AGCTTGCGCT	300
ACCTTGCTCG	CATCGCTCTG	CGATGATGATG	CGAACGGCGAG	GTGGCGACA	AACTGGCTCG	360
ACCGAGGTT	TGGCGCTTTC	CGACGCTGTC	TGGACGCGCG	GTACTCGCTA	TAATGCTCG	420
CCCCGA						436

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDENESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCGCGCA	GGTTGTGTC	CTCTCGCG	GGATTGCGA	TAATCTCGC	TGGGTGGACG	60
CGCCGATCRA	CTATGAGGC	GGACGGTAG	CTTTCGAT	ACCCACGCT	AAAAAATTIA	120
TCAAAGAAC	GAAGAAGTT	GGCATGAGCA	CTTTCGCGC	CTACCGCGC	ATGTCGCCGA	180
GGCGAACCGT	GAACGAGACC	ACGATGAGC	GTGGCGACG	GGGGCGCGC	GACATGCGA	240
TGGACATCGA	ATTCGGCGA	ATCTGGCTG	GGAGACGCA	TACGGCGCA	ACCGATGCGA	300
GGCAACCGAA	TTTACGCTGTG	GTGGCTG				327

## (2) INFORMATION FOR SEQ ID NO:248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly  
 1                   5                   10                   15  
 Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly  
 20                   25                   30  
 Ser Gly Gly Lys Gly Gly Ala Gly Asn Gly Gly Asp Gly Ser Phe  
 35                   40                   45  
 Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly  
 50                   55                   60  
 Gly Asn Gly Gly Lys Gly Gly Ala Gly Ser Asn Pro Asn Gly Ser  
 65                   70                   75                   80  
 Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly  
 85                   90                   95  
 Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala  
 100                 105                 110  
 Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser  
 115                 120

## (2) INFORMATION FOR SEQ ID NO:249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro  
 1                   5                   10                   15  
 Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe  
 20                   25                   30  
 Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg  
 35                   40                   45  
 Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Tyr Asp Leu Val Glu  
 50                   55                   60  
 Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val  
 65                   70                   75                   80  
 Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ser Lys Leu Thr  
 85                   90                   95  
 Glu Ser Leu Arg Leu Tyr Asp Ser  
 100

(2) INFORMATION FOR SEC ID NO:250:

CIVIL INGENIERIA CONSTRUISTECH

- (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350.

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile  
 1                   5                   10                   15  
 Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg  
 20                   25                   30  
 Ala Pro Thr Pro Pro Ser Asn Val Asn  
 35                   40

(3) INFORMATION FOR SEO IN NO. 253.

#### (4) Sequence characteristics

- (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

### (4.4) MOLECULE TYPES: *proteins*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251.

(2) INFORMATION FOR SED ID NO: 262.

#### **6. ASSOCIATE CHARTER STYLES**

- (A) LENGTH: 51 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

GENE MOLECULE TYPE: protein

## (a) STUDENT DESCRIPTIONS: SOC 10100

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu  
 1                   5                   10                   15  
 Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala  
 20                   25                   30  
 Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val  
 35                   40                   45

Gln Thr Glu Tyr Gly Gln Pro Asn Leu Pro Val Val Pro  
 50                   55                   60

## (2) INFORMATION FOR SEQ ID NO:253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

CTTTGGAGCC	CTCGGACGCC	GTGTTGGTTC	TGGGGCTGGA	TTCGTTTCTG	GGGAAAGTCA	60
ACTAAAGACC	ACGTTGACAC	CCAAACCCGG	CACCCGATG	GGCGGTGCGG	GGCTAGAAGC	120
TTCGACCGG	GCACGAAAC	TTCGTTGGTC	CGGGGGCTGC	AGATGGCA	CGCTTGCTTG	180
AACATGGTT	GGACCCGTC	GTACCGCG	GCT			243

## (2) INFORMATION FOR SEQ ID NO:254:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CGGGCTCT	TTTGGCCCC	GGCGTGGG	GGGGGGGG	TGGGGGGG	ACGGACGG	60
GGCCCGCTTC	TTGGGGGG	ACCGGGAC	ACGGGGGAT	GGGGGGGG	GGGGGGGG	120
TGGGACGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	180
ATGGGTTGGC	TTTGGGGGT	ACGGGGGG	CGGGGGGG	GGGGGGGG	GGGGGGGG	240
GGGGTGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	300
GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	360
GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	367

## (2) INFORMATION FOR SEQ ID NO:255:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGCGTGT	TGGCAGGGG	ACCGGGAC	GGGGGTAG	GGGGGGGG	GGGGGGGG	60
GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	GGGGGGGG	120
CTACTTGGC	GGGGGGGG	TGGTCA	TGGTCA	TGGTCA	TGGTCA	180

GTCCGCTTA TGGACCGCT GGGAGGCGC ATTGTCCAC CGCTTGGCT ACCCCCAGT	240
CCCGCGCGCA CTGCGTCGA CGGGCGCGA TCACGACCTA ACCGAAATCCG AGCTCGCCGA	300
CGCCCGAGCGT GACTTGAGG ACTTTCTGGCT CGCAGCGGCC CAGTGGACTT CACCGCGACG	360
TTTAAACGCC ACCGGCGCA CCTCGCGCA ACACATGCCT TACCGCGAGC CGACACCGTT	420

## (3) INFORMATION FOR SEQ ID NO:256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTTTTGCGG TGGCATCGCC GTTACCGCGG GAAACCGCGG CAAACCGCGT ATGGCGCGG	60
GGCGCGCGG GGGCGCGT GGGCGCGT TCAAGCTTAA CACTGGCGGT GGGCTTGGG	120
GGCGCGCGG GGGCGCGT GGGCGCGT GGGCGCGT GGGCGCGT GGGCGCGT	180
GTCACACGG CGGGCGCGGC GGGCGCGT GGGCGCGT GGGCGCGT GGGCGCGT	240
TGGGGCGCGG GGGCGCGT GGGCGCGT GGGCGCGT GGGCGCGT GGGCGCGT	299

## (2) INFORMATION FOR SEQ ID NO:257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Lys Glu Pro Trp Ser Asp Gly Val Gly Lys Glu Val Asp Ser Phe Ser			
1	3	10	18
Ala Lys Val Asn			
20			

## (3) INFORMATION FOR SEQ ID NO:258:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Gly Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Ala Gly			
1	5	10	15
Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly			

20	25	30																		
Val	Gly	Gly	Asp	Gly	Gly	Trp	Leu	Ala	Pro	Gly	Gly	Ala	Gly	Gly	Ala					
15																45				
Gly	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Gly	Ala	Ary	Ser	Asp	Gly	Gly	Ala	Leu				
50																55	60			
Gly	Gly	Gly	Gly	Gly	Gly	Thr	Gly	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Ala	Gly				
65																70	75	80		
Gly	Arg	Gly	Gly	Thr	Leu	Leu	Leu	Gly	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Leu	Gly			
																85	90	95		
Gly	Ala	Gly	Arg	Arg	Arg	Arg	Trp	Arg												
											100		105			110				
Ser	Gly	Gly	Cys	Gly	Trp	His	Trp	Trp												
											115		120							

## (2) INFORMATION FOR SEQ ID NO:259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Gly	Val	Ile	Gly	Lys	Ala	Thr	Ala	Gln	Arg	Pro	Val	Ala	Ala	Gly	Arg				
1																15			
Pro	Arg	Pro	Arg	Pro	Gln	Arg	Pro	Val	Ser	Asp	Arg	Val	Ser	Asp	Gln				
																20	25	30	
Arg	Arg																		

## (2) INFORMATION FOR SEQ ID NO:260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu	Val	Gly	Ile	Gly	Gly	Thr	Gly	Gly	Asn	Ala	Gly								
1																15			
Met	Leu	Ala	Gly	Ala	Ala	Gly	Ala	Gly	Gly	Phe	Ser	Phe							
																20	25	30	
Ser	Thr	Ala	Gly	Gly	Leu	Phe													
																35	40	45	
Thr	Thr	Gly	Val	Gly	Ala	Gly	Gly	Gln	His	Thr	Gly	Gly				50	55	60	
Ala	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Leu	Phe	Gly	Ala	Gly	Gly	Met					
																65	70	75	80

Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly  
 85 90 95  
 Ala Gly Gly

(3) INFORMATION FOR AGO ID NO: 261.

#### 4.3 SEQUENCES: CHARACTERS & STRINGS

- (A) LENGTH: 382 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### (15) MOLECULE SIZE: CHS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261

```

TCTCTTCGGG CGCGCGCGCG GTGGCGGTG TTGGCGGTGA CGCTTGCGCA TTGGCTGCGA
CGGGCGCGCG CGGGCGCGGT GTTGCCTGGG CGGGCGCGTG CGTGTTCAGC GTGGCGCGCG
CGGGCGCGGC CGGGCGGAATC CGATTGTTG TGAAACGCGG TGGCGGGGGG TGCGGGCGGT
CGGGCGGTGT CTGGCGCGAC CGCGCTCGCG CGGGCGCGCG TGGCGGTGG CGTCAATTACCG
CGGGCGCGCG CGGGCGCGAC CGCAACGCCA CGCTCGCTGT AA

```

(2) INFORMATION FOR SEC ID NO: 263.

#### (a) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

**1.1.1 MOLECULE TYPE: COMB**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263.

CCTGGCGGAGC	CCTTGCTTACTG	GTCATGATGAT	GCCTTGATTT	TGACCTTTGCC	GGCGCCCGGT	60
CAGCTCTTGT	CAGGACCCAC	GTATATTGCG	AARACCAATC	CGCGCGGCGA	GGCGGAGGATG	120
AATGCCACAC	CGCGCGCGAT	CAGGCGGGGG	AGCCACAAAC	CGATCGGAGC	CGCTGTGTCACC	180
GAGCCGAGA	ACCGCGGAT	GATCGGCGAC	CAGCTTATCG	CGCTGAAGAA	TCCAGTTCTT	240
CTTGGCGGAT	CGCTGATTTG	AGCGGTTTG	TAGTCTTGGG	CGCGGAGGATC	TAGCCCGGGG	300
GCCTCAAACC	CGAAGAAGGT	CGCGGACATC	AACGCCCTGC	CGCGCGTGAG	CGCGAACCGA	360
ATGGTGCGCG	CGCTTCTGAC	ACCGACGTTG	GGGAACATCG	AGGTGCAACAG	GGCGGT	420

(2) INFORMATION FOR SSO IN NO. 263.

### (2) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 373 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### (iii) MOLECULE TYPES AND

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263.

TCACCGCGTG AACGTTTGT AACACTGATA CTTATGGTTG TCAGCGACCA GATCAAGTCC	60
AGTCGGACCA ATGCCCGAGG ATCATCGCT AGGCTCACCG TTTCCGTTTG GACGGAGACGG	120
TATGGATTG TGCGCTTGA CGCTCCTCGG CGCGGTGCGA AGTGTGAGTC GGCATCGAA	180
CGGTTGCAA TACCACTTT TCGGGATAT GGCGTATTTC GTGTCGTTG GCTGATCAC	240
CCTATCGTT TTGAGACCTT CGCGAACGGC GGTCCAGTTA CGCGCTTTC ACTGGCGCT	300
CGCGTACGT CGCGCGCTCG ATCGCTTGA ACCTCATCGC AATTGCGCGA ATGCGTGACT	360
ACCTGAGCGT CCT	373

## (2) INFORMATION FOR SEQ ID NO:264:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCCGA CGCGCGCGA CGCGCGCTCG GAATTTGAC CACCGCGCGC GTCGCGTGTG	60
CCCAACGGT GACCACTTG TACGCGCGC ATGCTCGAT CGCGCGTTG GTGTCGTCG	120
GCGCGACTAC CGCGCGCGTC AATCGCGAGCG ACCAAAGCAA CGCGATCGAT AGCGCGATCG	180
CCACTCTGTC CGAAATCGAG CTGCGTGTAC AAGCTTGGG CGCGATCGAA ACCCGCGCGA	240
ATGATTGAGT TTAACTCGT TAGCAATTAAC TGGCTTACCG CCTTGGCGCG TCTTAACGGG	300
TCTTGAGGGG TTTTTCGTC AAAGCGGAA CGATATCGG AATACCTGC GTAGTAGCGA	360
AGCGCGCGC ACCGATCGT CTTCGAAAC CGTGCAGCG CGCGATCGCG AATCGCGCG	420
CCC	423

## (2) INFORMATION FOR SEQ ID NO:265:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATGGTCCGAC CGTCGCGCA ATGCACTCGAG CTCCCGTAC GTGAGTGTAC CGCCCGCGCGA	60
ACTGACCGCC ACCGATCGA GGTGTCGCGC AGCGATTTGG CGCGACCGCG TATGACCGCG	120
CGTTCGAC CGTGTGAT CGCGCGCGCG CGTGTGCGT CGTGTGCGT CGCGCGCGCG	180
CGAAATTCG ACCTCGCGCA CGCGCGATCG CGCGATCGCG ACCGATCGT GTGACACAGC	240
CGACGCGCG CGTGCAGCG TTTCGGCGC CGATGTGCGC ACCGATCGT CGACGACGTC	300
CACTAGCGAC CGTGCAGCG CGTGTGCGC GTGCGCGCG ACCGATCGCG CGAAGCTCGA	360
CGAACTCTGT AGCGCGCGCG CGCGATCGT CGCGCGTT CGCG	424

## (2) INFORMATION FOR SEQ ID NO:266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTCCTGTTGC CAGGCTTTC TTGGAAACCGC CTGGCTTAAC TGGCAACGGG GATGGTGCGC	60
ACCATTGAAAC CGGCCAACCC GCGGTTTCA CGCGCTACTT CGCAAGACCC CGCGCTTCA	120
GTGGGACCAAC TTAAGGCCCCA CGCGCGCGG GCACTATTGG ACAACGGCAC CGCGCGATTC	180
GTCGGCTTGC CGCGCGCGC CGAATGGCG CGACCGCGCA GCATCATGTT CTTCGATGAC	240
ATGGCGGTTG CACCGGGCGT CGATTTGTT CGCGCGCGG CGCGCGGTT GACCGGGCG	300
GACCAACCGA CGCGCTTCTT TGGCAACGGG CGCGCTACTT CGCAAGACCA CGCGCTTCTC	360
GGTCACACCG CACGATGAA TGTGGCTGAC CGACCGCGCA CGATTTGAC CGCGATCGCC	420
C	421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGGATATCA CGCTTCAACG CATTCTCTGT CGATGTTTGC GGCGCGCGCG CACGAACTA	60
CGAGGAGCTC CGCGCGCTAT TGGCGCTTG CGACCGCTTG CGCGCGCTTG CGCGCGCTTA	120
CGGAAACCCA AACCGGTTA TGGCGCTTT AGCGCGTGG CGCGCGCTGG CGATGGGGCG	180
CGCGCGCTTG ACACGCTCAT CGACGGCTC ATGGAAAGCC CGCGCGCGCA CGCGCGCTTC	240
CGCGCGCTGG CGACGTTTT CGCGCGCTTG CTGGCGAGCA TTGACGACGA CGTTCCATC	300
ATGTCGCGCA AGGACATGG CGACGAGCTC CTCACGTTGC TTGGCGCGCG CGCGCGAACG	360
ACGGGGGGCGA CGTGGCTTGC CGCGCGAC CGCTTCAACG CGACCGCGAC CGCGCGCTTG	420
CTCTGG	426

(3) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCCTGTTGC CAGGCTTTC TTGGAAACCGC CTGGCTTAAC TGGCAACGGG GATGGTGCGC	60
ACGTCGAAAC CGGCCAACCC GCGGTTTCA CGCGCTACTT CGCAAGACCC CGCGCTTCA	120
GTGGGACCAAC TTAAGGCCCCA CGCGCGCGG GCACTATTGG ACAACGGCAC CGCGCGATTC	180
GTCGGCTTGC CGCGCGCGC CGAATGGCG CGACCGCGCA GCATCATGTT CTTCGATGAC	240
ATGGCGGTTG CACCGGGCGT CGATTTGTT CGCGCGCGG CGCGCGGTT GACCGGGCG	300
GACCAACCGA CGCGCTTCTT TGGCAACGGG CGCGCTACTT CGCAAGACCA CGCGCTTCTC	360
GGTCACACCG CACGATGAA TGTGGCTGAC CGACCGCGCA CGATTTGAC CGCGATCGCC	420

CGGCGCTCGG AGCGGAAACT CGTGTCTGGGC AGGGCGAGATG GCGCCGTCCTTA CACGGTTGCC 480  
 AAGAACCCGC ATTTGACCCG CGTGGGGGGC GCGACCGTAG CC 522

## (2) INFORMATION FOR SEQ ID NO:269:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCTGGGGCCC AGCGGCGTCG GCGGGCGCA CGCGCGGGCG CGAGACGGCG CGCGAAACCA 60  
 ACCCGTGCC CTGAGGCGC CGCGCGCGCG CGCGCGCTGT CGTGTGTGTG TTGGGGCGCA 120  
 TCGCGATTCG CGTCGCGAT CGCGCGCGCG CGTGTGTGTG CGCGCGCGCG CGCGCGCGCG 180  
 AGCGGTTTG CGCGCGCGCG CGTCGCGCG CGTGTGTGTG CGCGCGCGCG CGCGCGCGCG 240  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 300  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 360  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 420  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 480  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 540  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 600  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 660  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 720  
 CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG 780

## (2) INFORMATION FOR SEQ ID NO:270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AAGACGTCGAGCGCGCGCA TCGCGCGCGCG CGAGCGCGTT AACCGCGCGCG CGACGCGCGTT 60  
 CGCGCGCGCG 69

## (2) INFORMATION FOR SEQ ID NO:271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACTGGACCCG CGAGCGCGA CGAACGATC GGTCGACTA GCACTGCCCG TGGAGCGCG	60
CGCGCGCTT CTGGCTTCCC AGCGGAAACG GTTGCGCGCG CGGGCTCAG AAGGGTTGGA	120
GGGAGAGTTG CAGGACCGTA TGACCGAGCG GTTCCCGCGT TTGGCTCGG CGCGCTCGCG	180
CGAAGGCGTG CGGGTCCCG CGACCGCATG GAGGTGGAT GTTCAGTTGA GTGGACTCGG	240
CGCGCCCGT CGGGCGATCG CTGGGCTACT GGCGCTGGCG CGGGGCGTTG CGGGAGCTG	300
CGGAGAAGA CGCGATCG TGTTCTCGA CGCGCGTAT ATCGGAGTGT CGGGCAATAT	360
TTCGCCCGCG CGCGCACTCG CGGGGTGCGA CGTCGCGCC CGAACCGCG CGCGACTCG	420
CGAGCAACCG CGGGCGATG AGCTGCTTCC GTTTCGCGCG CGCGCACTCG CGGGCGCGTC	480
CGGGCGCTCG CGGGCGATCG TGGTCTCGA CGCGCGCTCG CTG	523

## (2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 224 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

CTGGGGTGT CGTCGGGATA CGGGCAATT CGCGCGCGCG CGGGCGCGCG CGGGCGCGCT	60
CTGCAGAAC CGGTGGCGCG CGGGCGCGCG CGGGCGCGA AGGGCGATCG GATTCGCGCG	120
GGGGCGCG CGGGCGCTTG TGACCGCATG TTGGCGCGT CGGGCGCGAT ACCGCGAACG	180
AACCGCGAG CGGGCGCGCG TGCGGCGCG TGCGGCGCG CGAC	224

## (2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 521 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TTAACTGACT CGGGCGCTCG ATGGCGCGCG CGGGCGCTCG ATAGCTGCCCG CGGGCGCGCG	60
TTAACTGACT TTGGCGCTCG CGGGCGCTCG TTGGCGCTTG GTCCGAAACCC TGCGCGCGCG	120
CGGGCGCTCG TTGGCGCTCG CGGGCGCTCG CGGGCGCGCG ATTCGCGAGC CGGGCGCGCG	180
TTGGCGCGCG CGGGCGCGCG CGGGCGCTCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	240
CGGGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	300
TGTCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	360
CGGGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	420
CGGGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	480
CGGGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	521

## (2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCGAGGTC ATTGGCTGA ACAAAAGGAC CGCGCCGTAC AGCGGACGCC CGCAATTGTT	69
CTCGTATAG TCGGGTACA CCTGGGATC CGCGCGTGA CGAACCTTG CGCGCGCA	120
CGGAGGAGC CGTGGCGGC TCAGCGGGG TCAGAAGCT AGTGCAGGAC ATGCTGGCG	180
CGCGAAGCTT TTGACCGTC AGACTCGGCC TGGCGTCTT CGGAGGCC CGGATCGGC	240
CAGAGCTTG AGGTTAGGCC CTGGAGCTCA CGCGGAGGCC GTTGCGCAC CGAGTCAC	300
TGCTGCTCT TTTCACCGGCG CGCGAGTCG CTGAACTTGA CGCGCTGAC ATGCGCGCG	360
GTCACCCCGA AGCGCGCG CGTGTGGCG CGCTGCGCC CGCGAGGCC CGCGAGCTCG	420
TGCGCA	426

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

CGGGACACCG CGAACAAAGC GCGATGGCC TCGGGCGCG CGCGCGGCC GACCGGGCC	60
AGGGCGGCC CGGGCGCA CTGATGGTA CTGGGGCGCG CGCGGACAC CGGGCGCAA	120
CGCGTGTGTA CGGGCGCC ACCGTCGCC GCTGAGCG CGATGGCG CGCGGTGCG	180
CGCGATGGCC TGATGGCA CGGGCGCC CGCGTGTAC	240

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG CGCGCGTGC TTGGCGTC TGGCTCTGC ATCGTGGCC CGCGCGATCA	60
CGGAGGTCG GCCTTGTACT CGCTGCTCG AAGGTCAGG ACCACAGTG CGTTTGGCG	120
ATGCTTTTCG ACCTTGGCG CGACGCGCTG GACATGCGG TTGCGAGGC CGTGTATCG	180
TGGCTGGCG TAAGCGATA CTGTTGCG AGCGCGATCA CGGTTAAACA CCTGGGGCG	240
CTGGCGGCC AATGGGACCA ACAGCTGGA TTGGAGGGT CGCAACGAGA TGTGCTCGC	300
GTTCGGAGTG ACCTTGGCG CGCTGAGTC GATTTTACG CGTGGCGAT AGAGCACTCG	360
CGCGCGTTGC CGCTGCTCG CGCGCGGCC CGCGCGGCC CGTGTGGCG	420
CTTGGAAACGC TTGATGATGT AGTGTGGCG CGCGCGACTCC AGACCGCGCA CGACATCCAC	480
CGTGTGGCG TTGCGCGCA CGCTGAGTC CGCGCGGCC GAATGGGGC CGACACCCG	540
CGACACCGTG ATGCGCGTC TGGCGGGCG A	571

## (2) INFORMATION FOR SEQ ID NO:277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Leu	Phe	Gly	Ala	Gly	Gly	Val	Gly	Gly	Val	Gly	Gly	Asp	Gly	Val	Ala
1						6			10			14			18
Phe	Leu	Gly	Thr	Ala	Pro	Gly	Gly	Pro	Gly	Gly	Ala	Gly	Gly	Ala	Gly
						20			24			28			32
Gly	Leu	Phe	Ser	Val	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ile	Gly	Leu
						36			40			44			48
Val	Gly	Asn	Ser	Gly	Ala	Gly	Gly	Ser	Gly	Gly	Ser	Ala	Leu	Leu	Trp
						50			54			58			62
Gly	Asp	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Val	Gly	Ser	Thr	Thr	Gly
						66			70			74			78
Gly	Ala	Gly	Gly	Ala	Gly	Gly	Asn	Ala	Ser	Leu	Leu	Val			82
						86			90						

## (2) INFORMATION FOR SEQ ID NO:278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met	Pro	Pro	Val	Ser	Ala	Asn	Ala	Met	Val	Pro	Ala	His	Ser	Thr	Pro
1						5			10			14			18
Pro	Val	Ala	Asn	Ile	Glu	Val	Asn	Thr	Pro						
						20			25						

## (2) INFORMATION FOR SEQ ID NO:279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg  
 1                    5                    10                    15  
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala  
 20                    25

## (2) INFORMATION FOR SEQ ID NO:280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp  
 1                    5                    10                    15  
 His Pro Pro Asn  
 20

## (2) INFORMATION FOR SEQ ID NO:281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro  
 1                    5                    10                    15  
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro  
 20                    25                    30  
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro  
 35                    40                    45  
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg  
 50                    55                    60  
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp  
 65                    70                    75                    80  
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala  
 85                    90                    95  
 Leu Thr Ser Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly  
 100                    105                    110  
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val  
 115                    120                    125  
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala  
 130                    135                    140

## (2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly  
 1                       5                       10                       15  
 Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr  
 20                      25                      30                       35  
 Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly  
 35                      40                      45  
 Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp  
 50                      55                      60  
 Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn The  
 65                      70                      75                      80  
 Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp  
 85                      90                      95  
 Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr  
 100                    105                      110  
 Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg  
 115                    120                      125  
 Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp  
 130                    135                      140

(ii) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn The Ala Pro  
 1                       5                       10                       15  
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Glu Pro Ala Val Ser Pro Pro  
 20                      25                      30  
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro  
 35                      40                      45  
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg  
 50                      55                      60  
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp  
 65                      70                      75                      80  
 Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala  
 85                      90                      95  
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly  
 100                    105                      110

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val  
 115 120 125  
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp  
 130 135 140  
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala  
 145 150 155 160  
 Lys Asn Pro

## (2) INFORMATION FOR SEQ ID NO:284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro  
 1 5 10 15  
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Ala Val Val  
 20 25 30  
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro  
 35 40 45  
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala  
 50 55 60  
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser  
 65 70 75 80  
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr  
 85 90 95  
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro  
 100 105 110  
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser  
 115 120 125  
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala  
 130 135 140  
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp  
 145 150 155 160  
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala  
 165 170 175  
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr  
 180 185 190  
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln  
 195 200 205  
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys  
 210 215 220  
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys  
 225 230 235 240

## (2) INFORMATION FOR SEQ ID NO:285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1           5           10          15
Leu Asn Ala Leu Ala Tyr
 20

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1           5           10          15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
 20           25           30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
 35           40           45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
 50           55           60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
 65           70           75          80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
 85           90           95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
 100          105          110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Gln Leu Pro Gly
 115          120          125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
 130          135          140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
 145          150          155          160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
 165          170

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Val	Gly	Val	Val	Gly	Val	Gly	Ala	Thr	Ser	Pro	Ala	Gly	Ala	Gly	Ala
1							5				10				15
Gly	Ala	Gly	Ser	Ala	Gly	Thr	Gly	Ala	Gly	Ala	Gly	Gly	Gly	Ala	Thr
							20				25				30
Lys	Gly	Arg	Ile	Asp	Ser	Ala	Ser	Ala	Leu	Ala	Ala	Pro	Leu	Ser	Thr
							35				40				45
Gly	Leu	Leu	Ala	Val	Pro	Ser	His	Thr	Thr	Asn	Gln	Arg			
							50			55					60

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met	Ala	Asn	Thr	Gly	Ser	Leu	Val	Leu	Leu	Arg	His	Gly	Glu	Ser	Asp
1							5			10				15	
Trp	Asn	Ala	Leu	Asn	Leu	Phe	Thr	Gly	Trp	Val	Asp	Val	Gly	Leu	Thr
							20			25				30	
Asp	Lys	Gly	Gln	Ala	Glu	Ala	Val	Arg	Ser	Gly	Glu	Leu	Ile	Ala	Glu
							35			40				45	
His	Asp	Leu	Leu	Pro	Asp	Val	Leu	Tyr	Thr	Ser	Leu	Leu	Arg	Arg	Ala
							50			55				60	
Ile	Thr	Thr	Ala	His	Leu	Ala	Leu	Asp	Ser	Ala	Asp	Arg	Leu	Trp	Ile
							65			70				75	
Pro	Val	Arg	Arg	Ser	Trp	Arg	Leu	Asn	Glu	Arg	His	Tyr	Gly	Ala	Leu
							80			85				90	
Gln	Gly	Leu	Asp	Lys	Ala	Glu	Thr	Lys	Ala	Arg	Tyr	Gly	Glu	Glu	Gln
							95			100				105	
Phe	Met	Ala	Trp	Arg	Arg	Ser	Tyr	Asp	Thr	Pro	Pro	Pro	Pro	Ile	Glu
							110			115				120	
Arg	Gly	Ser	Gln	Phe											125
							130								

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Pro	Gly	Ser	Rhe	Ala	Arg	Thr	Lys	Pro	Pro	Gly	Arg	Thr	Ala	Asp	Ala	
1																
														10	19	
Pro	Ile	Arg	Cys	Arg	Asp	Ser	Arg	Gly	Thr	Ala	Gly	Ris	Arg	Ala	Lau	
														20	29	30
Asp	Glu	Pro	Pro	Pro	Arg	Gly	Ser	Glu	Pro	Ala	Arg	Arg	Arg	Ser	Arg	
														35	40	45
Gly	Val	Arg	Thr	Val	Val	Ris	Asp	Ser	Leu	Ala	Ala	Arg	Arg	Val		
														50	55	60

(2) INFORMATION FOR SEO ID NO: 290:

## 6.0 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 72 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:286;

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly  
 1 8 16 18  
 Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly  
 26 28 30  
 Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala  
 38 40 45  
 Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp  
 50 58 60  
 Arg Gln Arg Arg Gly Arg Arg Arg  
 68 76

(2) INFORMATION FOR SEO IN WORKS:

142 SEQUENCES CONNECTED WITH

- (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### MOLECULE TYPE: expression

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

Asp	His	Arg	Arg	Arg	Ser	Lys	Ala	Ser	Lys	Arg	Ser	Ala	Ser	Ser	Pro
1					5					10					15
Ala	Arg	Ile	Thr	Glu	Val	Arg	Pro	Cys	Thr	Pro	Lys	Lys	Glu	Arg	Ser
										20					25
															30
Ala	Pro	Gln	Ser	Gly	Ser	Arg	Asp	Pro	Phe	Arg	Pro	Trp	Pro	Ala	Asp
										35					40
															45
Ala	Gly	His	Ala	Arg	Ser	Pro	Ala	Trp	Tyr	Arg	Lys	Gly	Ala	Gly	Asn
										50					55

Phe Ile Pro Val Arg Ala Ala His His Glu  
ss 78

(2) INFORMATION FOR USE IN NO. 383.

142 [SEARCHES](#) [TOPICS](#) [ABOUT](#)

- (A) LENGTH: 174 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### (A) MOLECULAR TYPE: CRAB

(sci.) SEQUENCE DIRECTION: SEQ TO NO. seq

```

CCGACGCTTA CACCCGTAT TGGAGGAGC CCTCTGCTCT GGGCGGTTT TATCCCTTGG 60
GCAACGTTA TTGACGCCG GAGGCGACT CCTCTGGACG CAACTTGAA CTGAGGCGGT 120
TTTCACGGCA ATCAAACGGCTT CACGAGGACG TTGACGTTTG AGCGGAGGCG CGCG 180

```

(2) INFORMATION FOR SEE ID NO. 281.

#### **III. REFERENCES AND SELECTED TOPICS**

- (A) LENGTH: 404 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### **MOLECULAR TYPE: C200**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22.

TTCGAAACCG	GTTAACCTTC	CCCTCCTTGG	CGCTAGAGAG	TTTGTCTCAC	TTTCCTGTA	50
ATTTTCCCCC	GCACCCGAGC	ACCGTGAGC	TCTGCTCTCT	ACTGGAGGTS	CTGACCGGTC	100
CTTGGGCCAC	GATGGCCGTC	GAAGCTTCC	CGCGGGGGGT	CTTCGCTCTG	TTAAGCTCTT	150
TGTTTACCGG	ATGGGATGG	CTCTCTGGTC	ACCTCTTACAT	TCTCTCTTCG	GGCAACGACT	200
ATTCGACCCG	ACCCGGCTTC	CTTAAATGSA	CTACCTCTGG	ACCCGGCTTC	CATACTCTGT	250
TCCCGAAAT	GGTTGCGAA	CTACCTCTGT	CGCTGGCTCT	CTTTCGGGGC	GATGTCAGGC	300
TAACCTACCG	GGAGCTTCAA	CGACCTTACT	CGCTGGCTCT	CGTTGGGGC	GTGTCAGGC	350
		GGATTCGGCC	ACCGCTCTTG	CACT		400

(2) INFORMATION FOR SEQ ID NO:284:

## (E) SEQUENCE DIRECTED SYNTHESIS

- (A) LENGTH: 134 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser  
 35 40 45  
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp  
 50 55 60  
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp  
 65 70 75 80  
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val  
 85 90 95  
 His Thr Arg Phe Ala Glu Ile Ala Ala Gln Pro Asp Ser Val Ala  
 100 105 110  
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu  
 115 120 125  
 Ala Asp Arg Leu Ala Thr  
 130

## (3) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GCTTGGAGCG	CTACGAACTG	CCTTTTGC	TGCTTGTGTC	GGCCGCTTG	GACGCCAGG		60
CCACGAGAC	CCCGGAGGCG	CTTGGGAGAC	TGTTGGCT	GGGGGGGTTG	AAATACTTGG		120
TCTCTGGGCG	TGGGAAACT	TCCAACCGCG	ACTCGGCGG	CCTGTTGGC	AAACGTTTCC		180
TCTTGGCGCA	CCTGGGAGGA	CGGGGTTG	AGACCTGGG	CTTTTTC	GAGGCTTG		240
AGACGGTGG	CTTGGAGATC	CTTGGGTT	GGGGGAGTC	CTTCAGCG	ATGGGAGG		300
AATATCGGCG	GTTGGGCGG	AACTTACGG	TGTTGCGGA	GGGGGAGTC	CTCAATTG		360
TGGTGGCGCA	CGAGGCGCT	CCTGGTTC	CTCCGGTTTC	TGAGGAGTC	ACCTTACGG		420
ACCTTGGCTA	CGGGGTTGG	CGAACAGGG	TGAGGAGGC	ACCAAGGG	CTGATCGG		480
CGGGGGGGCG	CGTGGAGG	GGAGTGGCG	GGATGGCGA	CGCGAG			526

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTGCCCCCGG	TTATCTGGCC	GGCGGAACTTC	CTCACGTCGT	CTGAGACCCC	ACCGATGTCG		60
ATCAGGGCGA	TGCGCATGAT	GGCGGAACTTC	GGCACGAGCA	GGGGGGCAT	GGGGGGGCGAA		120
TAGACCGAATC	GGCGGAACTTC	TGCGGAGTC	GGCGGAGCA	GAAGAGCTGC	GGCGGACGATG		180
CGGAGGAAAC	TGCGGAGTC	ACCGATGTCG	GGGGGGCGG	TGACCTTCAC	ATCTCGGTC		240
CGCTTGGAGC	GGCGGAACTTC	GGCGGAGTC	GGGGGGCGG	TGACCTTCAC	GGGGGGCGG		300
TAGCTGATCA	TGCGGAGTC	GGCGGAGTC	GGGGGGCGG	GGGGGGCGG	GGGGGGCGG		360

CCCGGATAGG ACAGGGCGAG CGAACCGCGG GCAACGCCCG CCACATCGCT GGACATCGTGC	420
AGACGCTACT GCACCGACGT GAAAGCGCTGA ACACCTCGCG AACGTCGAC AGCTTGAC	480
ATTTGGG	487

## (2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 518 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCCCG AGAATATGAG CGGAGGAAAC CGGGCATTTA CGAGCTTGGG TTGCGGCGC	60
CTCAGCTTC GTCTTCCGAC CGCCCTGGTC CGCTTGGCT CGACGTTTTC GAGGTTTCT	120
CCGACCGCG CGCTGGATC CGCTTGGCG CGCCCGCTGC CAAGGCCGCC CTGGACACAG	180
ACCTGGTGC GTCTTCCCG ATGGATGAAAC TACTGGACTA CGCTCGCCG CGCCGTTAA	240
TAATCTTCAA GACGATCAT TTGACCGACT CGGATTCATC TGAGCTAAGC CTGTTACCG	300
TGGCGACAG CATGGGACC CGCTTGGCG TGCTTGCGG TTGGGACCG GAGCTTAACT	360
CGGAGCGTT CGACCGCC CGCTGATTC TGCGGATTCG TGCGGACCG CGTGGCTGTA CGGCGAAC	420
ATGGGCGCG CGACCGCCG GATGGCGCTT CGGACGACG GAGCTGATC GATGACTCT	480
CTTCCGACG AGCGACGAT ATGCGGATT TTGACCGCTT CGACGCTCG	528

## (2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 610 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCGACCGCT GAGGCGCCG CGCGCGCGT TGGCTCGCT CGGGCGCG CGCGCGCG	60
CGCGCGCG CGCTTGGCG CGCTTACG CGCTTGGCG CGTGGACCG CGCGCGCG	120
TGGCGCGCT GTTGGACCG TTGCGGCGG CGACCGCTTG CGCGCGCG CGCGCGCG	180
CGCGCGCG CGCGCGCG CGATGGCG CGCTTGGCG CGCTTGGCG CGCGCGCG	240
CGCTTGGCG CGCTTGGCG CGCTTGGCG CGCTTGGCG CGCTTGGCG CGCGCGCG	300
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	360
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	420
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	480
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	540
CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG	600
CGGGTGTAC	610

## (2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 164 amino acids
  - (B) TYPE: amino acid

(C) STRANGENESS: single  
 (D) TOPOLOGY: linear

### (4.3) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: seq ID NO: 2

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr  
 1                   5                   10                   15  
 Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala  
 20                   25                   30                   35  
 Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn  
 35                   40                   45  
 Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu  
 50                   55                   60  
 Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu  
 65                   70                   75                   80  
 Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr  
 85                   90                   95  
 Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His  
 100                  105                  110  
 His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro  
 115                  120                  125  
 Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu  
 130                  135                  140  
 Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala  
 145                  150                  155                  160  
 Ala Gly Ala Thr

(2) INFORMATION FOR USE IN NO. 200.

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANGENESS: single
- (D) TOPOLOGY: linear

MOLECULES TYPES OF POLYMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro  
 1                5                                  10                                  15  
 Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln  
 20    25    30  
 His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg  
 35    40    45  
 Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg  
 50    55    60  
 Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro  
 65    70    75    80  
 Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr  
 85    90    95  
 Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

100	105	110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala		
115	120	125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu Ser		
130	135	140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln		
145	150	155
Leu		160

## (2) INFORMATION FOR SEQ ID NO:301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu		
1	5	10
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu		
20	25	30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu		
35	40	45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser		
50	55	60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met		
65	70	75
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser		
85	90	95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Leu Ala		
100	105	110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg		
115	120	125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His		
130	135	140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser		
145	150	155
Ser Gln Glu Pro Gly Ala Ile Ser Asp Phe Glu Pro Phe Asp Leu		
165	170	175

## (2) INFORMATION FOR SEQ ID NO:302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr  
 1                5                10                15  
 Pro Ala Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro  
 20                25                30  
 Thr Val Pro Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser  
 35                40                45  
 Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro  
 50                55                60  
 Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala  
 65                70                75                80  
 Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr  
 85                90                95  
 Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg  
 100              105              110  
 Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly  
 115              120              125  
 Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His  
 130              135              140  
 Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr  
 145              150              155              160  
 Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro  
 165              170              175  
 Pro Leu

## (2) INFORMATION FOR SEQ ID NO:303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCGGGAC	GACGGGAAAC	AACACCGGCT	TGTTCGAATTC	CGGGCGATTC	ATTAACCGTA	60
TCGGGACAC	CGGGGTTTC	AACACCGGCA	GCTTCAATCC	GGGGCGATTCC	AACACCGGGG	120
ATTTCAACCC	ANGCAACTAC	CACACGGGGA	CTGCGAAAGA	CCCGCGATTC	TACACCGGCS	180
CCTTCATCTC	GGGCAGCTAC	ACACACGGGT	CTTGCTGGAGT	GGAAATTATA	ATGGCTCATTT	240
GGTTTACGCC	GGGGCTTCTGGA	ATTCCTTCTG	CCATTCTAAC	TCTCTCAACAA	GCTTGCGGCC	300
GCACTCAGC	CTGTTGAAAT	GATTCGGTTT	AACCGCTTAA	CAATACTTAG	CATAACCCCT	360
TTCGGGCTCT	AAACCGGTCT	TGAAGGGTTT	TTTGCTTAAA	GGGAAACTAA	TATCCGATA	420
ACTGGGCTTAA	TACGAAAGC	GGCACCGGATC	GGCTTTCCAA	CGTTGGCGCA	CCGGAAATGGC	480
AATGGACCCN	CGCTTCTACG	GGCATTAACG	CGGGCTTGTIN	GGGGCTTACCC	CGACGGTACCC	540
GCTTACCTTG	CGAAGGSCCTN	GGGGCTTCTT	TGCTTTCCTTC	CTTCCTTCTTC	CCGGCTTGGCG	600
GGTTTCTCTC	ACGCTTAAAT	GGGGGNNNNC	TTTGGGGTTTC	GGATTTATTC	TTACGGGCGC	660
CGGGCGGAA	ANNTTATTTG	GGTTTAAATTC	GGTTTGGGCG	GGGGGGGTTA	NTNNNNNTTT	720
TGGGGCTTAA	CTTTCGTTTTC	CTTCTTCTTAW	NTGAGCTTNT	TTCTCTCTGA	AAAGCTCTCC	780
CGTTTGGGSSG	TTTCTTCTTGA	WTAAATGGGR	AATTGCAATY	CGCGTTTGGG	TTWAAMTTAA	840
CGTATTTGCA	ATTTTCCGAG	TTTCTTGTATR	TTTENCXCGW	KGCTCCGKKA	SSGNTTTGGT	900
CCCCCTTTS	CGTTCCTTCA	6				921

## (2) INFORMATION FOR SEQ ID NO:304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTGCGGAG	GAGATAGGG	GGCAACGGGG	TCCGGAGGCG	GGGGGACCGT	GGCGGACAG	60
ACCGGGGTCA	ACAGCACCCG	GGTGGGTCG	ANGCAGAGGC	CCGGGTTGAT	GGCGGCGGAG	120
ACGGCGAACAA	CITGGCGTAG	CGTGCGGTC	GACTGGCG	TGGTGAGC	CATGGGCGG	180
CGGGCTGGCT	CGAACAGGCC	TTGGCTGTC	ACGGTTAGG	CAGGAGGAA	ACGGGCGG	240
GAAGACCCAG	CGGGGCTTC	CGGAGGAGC	TGGGGCTGG	ATGGCTGGG	CGGAGGAGC	300
CGATCGCTTA	GAGATGAGCC	GCTGGGGAA	GGCCGGGGCT	GGCTTGCGGC	AGGGGCGG	360
GCAGGGCGAC	CGGGGAGCTA	NGAACACGGC	AAGGAGTATA	ANGGCAACAG	CGATTTGCA	420
GGGCTAAAGC	CTTGACATCC	AGGGATTCG	GGGGGGCGAC	CGGTGGGTC	TCGAGGCGA	480
CGGCGTCTT	GGGGGGGAC	TGTCGAAGA	TCGGCATGAA	CAGKCTGAGT	CTTGCGGCGA	540
TATGAAAGG	CTTGAGCTT	TTAAAGCCGG	AAAAAAASTC	TCGGCTGGA	TAATATCGG	600
CGGGGAGGCC	CGGGTGGCGW	GGCTCYGGGC	ATTTTCAAC	GGGTTTNAAG	GGGGTTGCG	660
GGCAACTGGC	CGAATTTAAC	TTGGGGGTT	CGGGGGGTTA	ACGGGCTTK	NGGGGTTAA	720
AAAACCGGNC	TTTTCGTTGAT	TTGGGCGG	GGGGGCTTC	CGGGGTTGAC	CAGGTTTAC	780
AMCCCGGCGS	KGCGGCTTGS	GAACCGTTC	CGGGGGGTT	TTGGGTTGTT	AMGGGCGG	840
AAACCGGKTY	GGKTGCKRTN	WASSAMGCC	CGGGGGTTTT	TAAGGGCCAN	KGRAANGKTT	900
CCTGGGAAW	CGTGGGATTC	GGGGGGGTC	TTGGGGSSCN	TTTACGRTTN	NRGGGGGAC	960
AMWTTTTCNC	GTGTTTATTC	GGTGGGCGMN	AAAGGGTTTT	TTTTTGSSSC	STGGGGGNT	1020
GGGTTTANAN	AAASATTTTC	TTGGGGGGTC	TTGGGGGTTT	CGTGGGTRR	GGGAACTTCA	1080
GG						1082

## (2) INFORMATION FOR SEQ ID NO:305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTGGCGCG	AGTGATCGCG	CTGAAAGCGG	TACGGGGGCT	GGCTGGGGTC	GTGGGGAAAC	60
AAAATCGCTT	CGAAGTGGTC	TGGTGAGCG	CTGGGGAAAG	CGGGGGCGCG	GGGGGGGGCG	120
ATCTGATGGG	GGGGGGCGCA	GGGGGGGTC	GGGGGGGCT	GGGGGGGAT	GGGGGGGGAT	180
TTGGGTTGCT	GGTTGTACCA	GGGGGGGTC	GGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	240
GAAGGGAGG	GGGGGGGGAA	ATGGGGGGGG	TGGGGGGG	TGGGGGGG	GGGGGGGG	300
GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	360
GGGGGGGGCA	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	420
GGGGGGGGCA	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	480
GGGGGGGGCA	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	540
GGGGGGGGCA	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	GGGGGGGGCT	600

ANTCGGAAGT CCCGCCAAGA RCTGGGGGCC CGCGGAAAC WTAATTTAAR	660
CCCTAACMWA ACTTMMNACC CTTGGGSCCY AAMGTTTTR AGGTTTTCTT MAAAGAAASA	720
ANTCGGAAGC CGGTGTTACO AAAAAACGCK CGTTGTCG CCGATTGSC NCGGAANKSA	780
AAGCCCGCTT TCGCNNNNC CGGGGGGT KGGTTTCCG MTCGNNWTTG CGCGGAACON	840
CTTGTSSNYGC CGGTCCCCG CTGGGTTCC CGACCGTACG MGGCCCGTTC GCGCCGCGT	900
YGGCCCGCCG AAGGNNNGGG MGGACGTTTG CGCGGAAKGG TCGGAAATGA MCGCTGAGTA	960
MTCGCGGAAK ASMGCCSNCC NGCGCGCGCG	990

## (2) INFORMATION FOR SEQ ID NO:306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTGGGTG CGAACCGGG CGTGTTCGG AACGGGGGGG CGCGGAACTC CGGTGGCGCT	60
GGTGGGCGG CGGGGGCGGC GGGCGGTACG CGCGGTTGGT TTGGTCAGG CGCGGCTGGC	120
GGTGGGCGT GTGTAAGTCG CGGGGGGGG AACGGGTTCA CGCGGAACTC CGATGGGGCG	180
GGTGGGCGT CGCGGTCGGA CGACGTCTGT CGCGGCTGGT CGG	223

## (2) INFORMATION FOR SEQ ID NO:307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTGGGGCG CGGGGGCGAA CGGTGGCGAC CGCGGAACTC CGTTGGCAC CGGGGGGGCT	60
GGTGGGCGG CGGGGGGGGG CGGGGGGGGC CGGGGGGGGG TGATGGCGA CGCGGCGGAAAC	120
GGGGGGGGTG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	180
GGGGGGGGTG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	240
GGGGGGGGTG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	300
GGGGGGGGTG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	360
GGGGGGGGTG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG CGGGGGGGGG	418

## (2) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTGGGCGC	AGGGAAACG	ATCGCATACA	GGCTTGCGG	CGAATCGGC	CGATACAGCA	66
GCTCGGACA	CGGAGACGA	CGATCGGGG	TCTGGCTTC	CGCTTGCAC	ACCACCGGT	120
TACCGGGCAC	CACCGGGGC	ACCGAGTCG	ACGAGTTAA	CGTCATGGG	TAGTTCCAC	180
GCAGGATAC	CCCCAACAG	CGCTCGTT	GAATGGACAC	CGTGGTTTG	CGTATCGCG	240
CGAGGAGCG	CTGCGCTTA	CGGGGTTCA	GCAGGTCAC	ACAGACTGCT	GCSTTATAAT	300
TACCGGTTAC	CGGATCGAT	CGACAAATT	CGCTTGCGC	CGGATCGCG	CGTGGCGCG	360
CTGGGTTAC	AGGAAAGTCG	TCGAGLACTC	CGGGTTCTG	ATNAACGGT	CGGATAGCG	420
CGGGATGACT	CGAGCTGCT	CGATCGGGG	ACCTTCGCA	TCGGTCTOC	CGGGGGCGA	480
CTTCGCGAA	TGCGGTTTG	ACTTCGCGG	CGCTGCCAAC	CGAATCTAT	CGGGTTTGC	540
CGTTAAAC	TCTCAATGT	TCGAGTCGA	ATTCGCGAAC	TTCTTATCCC	CGGCGTTC	600
AACGAGCGA	ACCTCGCGAA	CGTTAGGTT	TCGCGCTCTT	TCGAAATTC	CGGTTTGCN	660
CGAATTCG	CGAGATGCTG	TCGAGCTGTC	CGATCGGGG	CGTGGTCTG	TCGAGGCGAK	720
CGAAAGGCT	TTGGGCGGG	CGTGGCGAA	CGTTCACCTG	TCGAGGCGA	TCGAGGCGCG	780
CGGAGGCGA	ATTCGCGAA	CGGGGGGGG	CGGCGATTC	TCGAGGCGTC	TCGAGGCGTC	840
TCGAGGCGT	CGAAAACGCG	CGGAAATT	TTTTTCGCG	TCGAGGCGAC	TCGAGGCGAC	900
TCGAGGCGG	CGGCGCTTT	TCGAGGCGT	TCGAGGCGT	TCGAGGCGT	TCGAGGCGT	960
TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	1020
TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	TCGAGGCGG	1080

## (ii) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTGGGCG	AGGGAAATCG	AGTGGTGAAG	CCTGGCTGG	TGCGCTTACG	66
CGAGAATCA	CGGTGACCGG	CGCTGGGTC	CGTATGCTG	CGCCGACCGG	120
AGGGCTGGG	TGCGCTTACG	CGAGCTGCT	CGATGCGAA	CGAAAGGCTG	180
CGAGGATACG	AGCTGCTGCG	CGCTGGGTC	CGCTGGGTC	CGATGCTATT	240
CGGGCTGGG	ATTCGCGAAC	CGCTGGGTC	CGCTGGGTC	ATTCGCGAAC	300
TTGCTTGTGG	CGAGAGCTG	CGGGGGCTG	CGGGGGCTG	TTGCTTGTGG	360
CGAGGATACG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	420
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	480
TTGCTTGTGG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	540
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	600
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	660
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	720
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	780
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	840
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	900
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	960
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	1020
CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	CGGGGGCTG	1080

## (ii) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCCGAC GAGATCATGA ATAGCGGCT GTTCAGCCTT GAATGGTGC CGCGATTCAGC	60
GAGCAGCTCT CTTCGTGCTG CCGAGCAGA GTTCGGCAGC GATCGGAGCA CCTGGCGATGT	120
CTTGCGATGT GTTCAGTTGC AGCTTGGCC GAGGCCGCGC CTTCGGTACG AGGGTGTCTT	180
GGCTTCTTCGC AGCTTGGCTA ACCCTAACTT CGGAGCGAGA CCAACTCGG CGCTCGATCC	240
GGCTTCCGGG CTTCGGCGGA CGCGGCTT GTGGCCGCTG GCGCGAGGT CGCTGGTGT	300
CGCGATGAAAG TAAAGAACCG CGCCATGCCG GTGGCGAAGT ACCGACTGACT CGCGAACGA	360
ACGATCGTGC TGTTCCTGT CGGGGTTAATC GAGCCGAGCA ACCGGGAGG CGACCGATCA	420
TTCGGATTGG CGCTTGACG GACCGACTTC CTTCGCGAGA CGGCGAGGGA ATGGTGTGTC	480
TTGGCGCGGG CGCTTGACG ATTCAGCGCG ACCGGCTGGC CGACGAGCCG GCTTACGCTT	540
ACATTAACAC GCGTTCTGC CGCACATTG CGGGTGTGCG CGCTTGCGAA CGGAAVAGC	600
CGCGATTCTG AACGAAAAAA TTGGCGCATY ARNGTGTGCG CGAAAACCGT ANTCCCGCTA	660
TCGGCGGGG CGGCGCGCTT NNNAAGACCG CGGAAVAGC CGCGCGCGCC CGGTTTGT	720
CCCGTTGTCG CGCGCGCGCG TTGGTGTGCG CGGCGCGCTT CGGCGCGCGCC CGGTTTGT	780
AAAAAAYCNG NCAGTAAAGA CGCGCGCGCG ASKTCGGCG CGCGCGCGCG CGGAAVAGC	840
ANTTAACGCG KAGAAAAAGN NCAGGAGCGCG CGGCGCGCG CGGTTTGTGG CGTGTGTTAG	900
AGAAAATTCG CGAGATCGCG TTGAAAGAA AGCGCGWCG CGCGCGCGCG CGGAAVAGC	960
GGCGTTGCG CGGCGCGCG CGGCGCGCG CGGCGCGCG CGGCGCGCG CGGAAVAGC	1020
CGGTTGCG CGGCGCGCG CGGCGCGCG CGGCGCGCG CGGCGCGCG CGGAAVAGC	1080

(3) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGAC GAGTGGATG GATCGAACAC CGCGCGACGT CGCGCGCGCG CATGGGGCG	60
CGCGATGGCA AGCGTCTTCG CGCGCGCGCG AATCGATTCG CGCTTCGACG CGAACCGCCG	120
AAACCGCGCG CGCGCGCGCG GATCGAACAC CGCGCGCGCG ATCGAAATAA CGTCCGACAT	180
ATAGAGACG TGCGCGCGAG AGCTTGGAG CGCGCGCGCG CGCGCGCGCG TTAGACGTGT	240
CGTTTGTGCA AGAAGCGCGT TGCGCGCGCA AGATCGACCG CGCGCGCGCG ATCGACGCAA	300
CGTTCGCGTG CTATCGCGCGT AACGTTGGCG CGCGCGCGCG ATGACGCGCG CGATTCGCG	360
CGCGCGCGCG ATCGACGTTG CGCGCGCGCG CGCGCGCGCG ATGACGCGCG TTATCGCGCG	420
TCTCGTGGAC ATCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	480
CGCGAAATTCTT TTCTCGCGCA AAACACTGCA TGTGCGCGCG CGCGCGCGCG CGCGCGCGCG	540
ACAGCGCGAA TTGAAATTCG CGTGGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	600
TGTTGCGCGAA AAATCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	660
AAAAGGTGCA AGCTTGGAGG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	720
WWTTGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCGCG	780
CGCGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCG CGCGCGCGCG	840
CGTTTAAAC CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	900

AAGGTTTTCG GCGAATCAA AAATTTTCA AAGCCCGAGK SARGGGGRTY TTNEAGGCGG GTYCCCCCOW YCGGGGCGNA KAYAAAGK NGSGNGGAAT NTNTTTTAKK EEEERNNNTT TYNTCTCTCN CGGGNRRWNG GRANNTGNTS NSSGGGSGGC	960 1010 1060
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## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTGGCGAC GAGCTTGACT AAAGAGGTGA CATGCCCTAT GATGCCACAT CGCTTGGG GCAATACGGG CATTGATGAA CTGAAMGGAN TCTGGGTTTC GTCGAACTGG ATTACGTTG CCAAAGTGAAC AGGCTTTGGG CGGAAAGATG CGACCTTAA CTGGCGCTTC CACCTGCAA TGTGTTGATG GATGCTGGAA CGGGCTGAC NGATAANGAA TTGGCTGGTC GGCGGGGAG ATGGATGTC CGTGTGTTGCT TGCGGCGTA AATTCGCTTGT GCAATCATCG GCAGGTTATC TTCCCGCTAC ATTCAGGATG TGCGGCTAAC GAAGAAGTTA TGACATGCG CAACGATTC CGGATCGNC CGGGCAATTT CGGACACCTGC TGTGTGTTGAA CGCTTGTGAC GAAATGGGGG GCTYAAAAGC NGCTTGCGT TGATTTAAC CGAACGTTTCA CGATGTTTC CTTGCGGAGTC CGTGTGTTGCT AACTGGGGG TTGGCGCTTC TGAAACTGAA CTGCGGCG TTGGCGCTTA MTGTTTCAA AAAGCGCTTA ACCGGAAATG AAACGTTAAC TGAAATGAA GAATCGGGC TTGGCGCTGC CGCGGAAAYN TTGCGCGCG CGGTGTTGCTG CGTTTGGCG AAACGTTG CGTTCGNNN TTGACGAGGCG MCNTTGTGCG CGGGGMMAS CGGGGGGGK TTTGGCGCTG TGCGGCGCTG CGGTGTTGCG CGGGGGGGCG CGGGGGGGAA AAAGGAGGAA CGGCGGCGCG CGGGGGGGG GAGTGGGGCG YKTRAAACAA ACCGGAAAGA TTGGCGGGC CGACCGGNNN GYGAAGAAGT TGNTTGTGAA MCNTTGTGCG CGGGGGGGK MCNTTGTGCG TTGGCGCTG AAAGGAGGAA CGGGGGGGCG CGGGGGGGAA NGAGGAGGAA CGGGGGGGCG MCNTTGTGCG MCNTTGTGCG CGGGGGGGCG CGGGGGGGK MCNTTGTGCG CGGGGGGGCG	60 120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080
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## (2) INFORMATION FOR SEQ ID NO:313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTGGCGAC GAGGAAAGG CGGGAAATGG GATGGGGCG AGCTGGGGCC CGTCGTTAAC GAACTTGGG CGAACTGGCG CGGGGGGGT CGGGGGGGT GGGGGGGGGT ATCTGGGGCG AGGCTGAACT CGGGGGGGAGA TTGGGGGGT TTGGGGGGCG TGGCTTCAAG TTGGGGGGAG TTGGGGGGCG TGGCTTCAAG CGGGGGGGAGA TGGCTTCAAG CGGGGGGGCG CGGGGGGGAG AGGCTGAACT TTGGGGGGCG TGGCTTCAAG TTGGGGGGCG CGGGGGGGAG TTGGGGGGCG CGGGGGGGAGA CGGGGGGGAGA TTGGGGGGCG CGGGGGGGAG TTGGGGGGCG CGGGGGGGAGA CGGGGGGGAGA TTGGGGGGCG CGGGGGGGAG	60 120 180 240 300 360
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## (2) INFORMATION FOR SEQ ID NO:314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTGGGAC GAGAGACCGG GTGGTTGACC AACGGACGCT TGGGCGCGG	60
CGCATCGGCC CTTCCTCTTC TTAAACCCCT AACGGCTTGC TGGCTTTTG	120
CACCTGGGT ATCCAGCCGA CGCGGATGA TGGTGGGC CACACCGGGT AGGTCTTCA	180
CGCGCGCGC CGCGACCGAC ACCATGGAGT GTCTTGCAG GTGTGGGCC TGGCGGGAA	240
TGTACCGCTT GACCTGAC TGAATCTCA CTTCACCGCG GAAACCTTCC GAAACCGCGA	300
GTTCGCGCTTC TTGGGAGTG TGGCTGTGC CG	332

## (2) INFORMATION FOR SEQ ID NO:315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTGGGAC GAGTCGGTCT AGACGGATTG AATGCTCCG CGAGCGCTTC GGCCTTGCGAC	60
ACCGCTCGAGC AAATATGCTT CAATGTGGTG ALCGAGCCCT TCGAGACCTT CACCGGGCGG	120
CGCTGTATCG GCAACGGGGC CAACGGGGT CTTCGACCG CGCTGTACGC GGGGGCGGGG	180
GTTGGCTGTT CGCGACGGG GGCACGGGG GTTGGGGTC GAAAGGAGT AACGGGGGGG	240
ACUTGGGGAC CGCGCGCGCG GATTTCTTC GCACTGGGGC ACCCGGGGGT CGCGCGCGT	300
CGCAGCAGGG CACCGGGGGG GACGCGGGCG CGTTCGGGG CGTCTCTGGT GGGGTGGGC	360
GTTAACGGG CGCGCGCG CGCGCTTAC CGCGCTTGGG GACGCGGGG CGCGCTTACCG	420
CGATCTTCTT CGCGCGCG GAAACCGGG CGCGCGGGG ACATTAAACCG CGCGCGCGAC	480
GGGGMCCCC CGCGACGGG GGYTTTTTC AACCGGGGGG CGCGCGGAC CGGGGGSTGTT	540
CGTTGGGGG AACGGGGTAC CGCGCTTACG TTAATCCCCG AAGGGTACMC ATSATGSNC	600
MTTTGGAA CGCGCGACAT TTGGGACCG CGCGCGGAAA ASGGGGTACG TGGGCAAACNA	660
MTTNCCTTNN NTTKGNNNA AAAANCCCTT CGCGCGACT NCGCCCGGNG GRGNCNNTNN	720
TTTTGGNNNN CGCGCGKAAM NTTCATTTTC NGGGGGNTNN CGGTTMMNNNA AACCCCGAAAM	780
MTTNNKOSCA AAGGGGGG NGGGGGNGGT TTTTCGNNRA MNNWTTNNNN NTGNGAASEN	840
NAAMCNNSME NGGGGGNNKA ARNNTTTWKTH KNSCNNNNN GGGGGGGGGG CGGGGGGGGG	900
MTTNNNANENG NGGGGGNNKK NGGGGGAAAA AACGGGGCKS NGGGGGGGGGG NGGGGGGGGG	960
GG	962

## (2) INFORMATION FOR SEQ ID NO:316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	AGAAAGACCC	CCGAAAGTTT	GGGCTGGCTC	TACGACTTCA	TCAGCGCA	60
GGGGGAAACG	AACCTTGCGA	AGATCTACGT	TGCGTTCCCC	GAAGCGCTCT	GGATGCGCCA	120
GTACCTGGCC	GCACCGCAGG	GGAACTTGAC	CCAGGATCGG	GCGGGAAAC	GGCTTGCGTT	180
GCAGA&gt;ATG	TGTTTGAGG	TGGCGTGGAG	GATTTTGCGAN	GGCGGGCG	TGACCCCGAAC	240
GGGTTTGCTG	TCGGCACTGC	TGCTCACCCAC	GGGGGGCGCC	GGCTTGACT	GGACCGAGCTG	300
CACCGCTGT	GGCGCTGTC	CCG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGGCAT	GTGTGTGCGC	GGGTCGAGAA	GAAGTGTAC	GGGACACATG	CCAGCGCGCG	60
CGCGCTTATG	GTGCTGGTGT	TGCGCGACCA	GGCGATCATC	ACCGGCATAC	AGCCGGCGCG	120
GGGAGTTCAC	ACCGGTTTGT	GTGACCTGCG	TGCGTTGAGC	CAAAGCGCTGT	AGACRAACAC	180
ATTAACCGCG	ACCGTGTACCA	GGGCCAGGAC	GGCGCCAGG	AGGTTGCTTG	GGCACCGATG	240
GGGAGAGAAC	GAGATGACCG	TGACGCTGCG	GGGATGCGCA	AGCGTTTGCG	GGTGGCGACC	300
GCTTCCCGCG	CCAGGGCGCG	GGCGGCGTT	GGTTATCA	GGTTGCGCGAT	ATGGGGCGCG	360
GGGACCGATT	GAGGCTTGTTC	GGCGGGCGCG	GGGTCATCAT	GGGGCGGCGA	ANCGTTTCA	420
GGCTGAGCGA	GGGATGATCG	GGGGGGCGCG	GGGGCGGCG	GGGGCGGCGA	ATGACTCGGT	480
GGGAGATTCG	GGGGCGGCGT	GGGACGGCGG	GGATGCGT	GGGGCGGCGA	ATTTTAAACG	540
AACTACGTTA	GGGTTTGGCG	GTCTTAACCG	GGTTGAGG	GGTTTGGCG	TTAAAGGAAG	600
AACTATTTTC	GGATGAGCGG	GGTGGTAAAC	GGAAAGCGCC	GGGGCGGCG	GGGGCGGCG	660
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	720
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	780
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	840
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	900
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	960
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	1020
GGGCGGCGCG	GGTGGTAAAC	GGTGGTAAAC	GGGGCGGCG	GGGGCGGCG	GGGGCGGCG	1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

AATTCGGCAC GAGGCGACAT CCCGGGGCCC TGTGTCATG ACTGGTTCTT CATGCTGAC	60
RAGGCACAGT CGCTGGAGCG CAAATGTTTG CTGACCGTCG TGTGGCTCTT CGGGACCGT	120
TCCGGCTGG TGTTCACCA CGACATGCC CGGGGGACAA ACCTGGGGT CGGGGGCCAC	180
GACGGTGGC CGCGGTGAGC GAGAAGCTCA AAGGTCATCC GTTGGTCCGC GAGTCACCT	240
TACTGGCGAG TGAACCTCC CGGATGCCCG CGCTGTCAC GAGATGCTCG AAGAGATCAC	300
CGGGCGCGC TGAATGCCCG TCCGGGGAGC A	331

## (2) INFORMATION FOR SEQ ID NO:319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AATTCGGCAC GAGATGCTCA CGCTGGAGAC CGTGCGACCG AGGGACGCC ACCAGTTAC	60
GCTGTTGCGC CAGAACAGTGG ACCAGGTGTT CGCTATGCGG CGACCGACAC TGAAGTGG	120
CGACGGAGTC CGGGTCTCA CGTACGGCGA TGAATGGTG TTGCGCATCA CGCTGACTA	180
TGACGGCTGG TCCGAAATGC AGCGAGCTGT CGACGGTACG GAAGCTGGTG TGGCGCTCTT	240
CGTGGCGCTC AAGGACATT CGCTGCTGT GTTACAGCG ATCGCGTAA CGCTTCATCC	300
CGCGCGACCG CGACGGGGCG CGGGCGCTTG TGCGGAGCG CGAAGGGCGT	360
CGCTGACCGC ATCGCGTGC CGGTTAACCC CGTGAGACG TGGCTGGTGC CGAAGTTGGG	420
CGCTGGTACCC ATCGATCGCG CGGGCGCTGA CGACGGTCTG TTCCACACCA CGTGGACGNC	480
CGGCGCGGAA CTGGTCCCGC ATMCAGCGA ATTCGTTGCGG CGACGGTGT TTTCGGTGT	540
GGCTTAAGCT TCGATGTTTGC CGCGCGTGT CGCGCGTGT CGGGCGCGCG ATCTTTCGAA	600
ATCGGSMSSAA ATCGCGCGCG AAACCGCGCG CGCTGGTGGG CGGGCGCGCG CGGGCGCGCG	660
AAACCGCGCG CGCTGGTGT CGCTGGTGT CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	720
CGCTGGCGCG CGCTGGTGT CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	780
AAATTCGCG CGGGCGCGCG CGCTGGTGT CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	840
TGCGGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	900
CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	960
CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	1020
CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG CGGGCGCGCG	1026

## (2) INFORMATION FOR SEQ ID NO:320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTCGGCAC GAGAAGACCG CGGGCGCTT CGCTGGCTC TACAACCTCA TCAAGCGCA	60
GGGGGAAACCG ATCGCGTCA AGATTTACGT CGCTGGCTCG CGAGCGCTGT CGATCGCGCA	120
CTACGGTGC CGACGGCGAC CGAGGCTGAC CGAGGATCG CGGGCGCGAC CGCTGGCTT	180
CGGGCGACG CGGGGGAGG CGGGGGGGG CGGGGGGGG CGGGGGGGG CGGGGGGGG	240
CGGGGGGGG CGGGGGGGG CGGGGGGGG CGGGGGGGG CGGGGGGGG CGGGGGGGG	300

GCACCACTCG TCCCGCTCTG GCGG

324

## (2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AATTCCGGAC	GANGCTGCC	GCTNAACAGC	ACCCCCCGGC	TGCCAGATAT	CCCCGACTCG	60
GTAGTCGCC	CCTGGCGTC	TTTGTCTCTC	TGACCGGGCG	CCGGCACCAT	AAGGTGGCTM	120
ATGCCAGGT	AGCGCCCGAG	GTGCGATGAG	TGGATGATGA	TGGACTTC	CAGCTCGCG	180
ACCGGGACT	TGGATCGCG	CCTGACGAG	AGGACGCGCT	AGGAAACATTC	GATCGATATC	240
ATATGGCT	CCAGAGTGGC	CCTGCGATTC	CGCGGTGCTC	CACCGAAAT	GCCTTGATT	300
CTACTCGCG	TATGTTTCCG	GCATCGCTG	CGGGATGAAT	GGAAACCGCA	GGATGGCGAC	360
GAAGGGCT	GAGCTGAGGT	TTCGTTTTC	GGCGACAGTG	GTGACACNC	GTTACTCGCG	420
ATAMATCGG	CCNAAAATCG	CGCGGAGCG	CGCCCAACAT	AANACCGGGC	ACNACAAATCG	480
CGGGCGCGT	CACTTAAACA	ACAGCTTGGC	ATCGGATTTT	GTCCCGCANC	CTCGAACCGT	540
CCCGAACCCC	TCTTCCCGCG	NACTTTTCTT	NNAAATTAATG	CCCGTTTGGK	CCCTGGCGCA	600
WTAAATGGGA	AACCGTTTCCG	GCACCTTCAA	GGGGTTGTTG	NAATTAACTT	GTTAACCGCG	660
AATTNTTCCG	GATTCGCGT	TCCTGGTTT	TTTNTTCCCG	ACCTTNGNN	GGGGCGCGCA	720
AGSTTTTCTT	SYTGAGCGG	GAACCCGAC	TTTNTTTCNN	AAACCSGNNAA	NTNTTTCGG	780
NNAAASGNT	CCCGTTTAAC	CACCGGCGT	AAACCGTMMG	NGGTTAAAAA	GGGSKNNETG	840
NGGCGTMMG	GGGGGAA	TSTTCTCNG	GGGGCGAAAW	ACGMMWGN	GTGEEKNNGG	900
GGGAAATTTT	ATTCGAGCT	GGGGCGSSGA	NTTNTTAAAG	MSCCCCCGNN	GTTGKCCCGS	960
TTTTGCGNAA	NNNGGKNNNN	GGGGCGNN	GTGNGGNN	NNAGCGGCG		
					1010	

## (2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATTCCGGAC	GANGCTGCC	GCTNAACAGC	ACCCCCCGGC	TGCCAGATAT	CCCCGACTCG	60
GTAGTCGCC	CCTGGCGTC	TTTGTCTCTC	TGACCGGGCG	CCGGCACCAT	AAGGTGGCTM	120
ATGCCAGGT	AGCGCCCGAG	GTGCGATGAG	TGGATGATGA	TGGACTTC	CAGCTCGCG	180
ACCGGGACT	TGGATCGCG	CCTGACGAG	AGGACGCGCT	AGGAAACATTC	GATCGATATC	240
ATATGGCT	CCAGAGTGGC	CCTGCGATTC	CGCGGTGCTC	CACCGAAAT	GCCTTGATT	300
CTACTCGCG	TATGTTTCCG	GCATCGCTG	CGGGATGAAT	GGAAACCGCA	GGATGGCGAC	360
GAAGGGCT	GAGCTGAGGT	TTCGTTTTC	GGCGACAGTG	GTGACACNC	GTTACTCGCG	420
ATAMATCGG	CCNAAAATCG	CGCGGAGCG	CGCCCAACAT	AANACCGGGC	ACNACAAATCG	480
CGGGCGCGT	CACTTAAACA	ACAGCTTGGC	ATCGGATTTT	GTCCCGCANC	CTCGAACCGT	540
CCCGAACCCC	TCTTCCCGCG	NACTTTTCTT	NNAAATTAATG	CCCGTTTGGK	CCCTGGCGCA	600
WTAAATGGGA	AACCGTTTCCG	GCACCTTCAA	GGGGTTGTTG	NAATTAACTT	GTTAACCGCG	660

AATTNTTCGG GANTCCTCN KCCCGGGTTT VSTNTTCCCC ACCTTINAN GGGCCGGCA	720
AGSTTTTCTT SYTGALGRRG GAAACCCRAC TTNTNTTYIN AACCSMNSA MNTTTTCG	780
MVPLASCONET CCCTTTCAC CAGCGGGTN AACCGTINNG NGCTTAAGAA CGGSIGNRIG	840
NCCTTMYANG CGGGGRANAA TSTTCNNICG GGGCXAAAN ACCCTTINON GTKKEENKSS	900
GCGAATTTT MMRAACTTEN GGGCCSSGA MTTTINAAAG MCCCCGCGN ESTGCACCGN	960
WTTCNNAA MMTCGCGNN STINCGCGN GCGGGCGNN MMAGMCGCG	1010

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

NCGGGGCGNS NTCAUCAYCA YCACGGGYW CWAATTCGGC CGCANCTTGT MLASAGATTT	60
CCTTATCAGC AGGAGCGATT CCTTTCAGAC GCTTTCGAAN CCAATRAGGC CTRATAATTY	120
CAACTCCACA AAAAACCGGTT GTCRATATTG SCGGRAAATR AAGGCGCCCG TMTCAACNYC	180
GCCTGGTTCY CCAATTCCCG TTTTGTANET CGCGGCTTAA AAAYCCCCCG TTTGGAYCC	240
CGGATGAA ACTGCCGGKT TAAAGTCTC GTTTTTGCGA TCCGGMMATT GAMSTCRGCG	300
ATTAAGAAAAC CGGKTTTGN CCTGSGNUTG CGAAATGCG AFGCGATAYC CGATGGCTG	360
KYCTTCTTCA YCGTAAACCA AAYCTGGGTA TCTTATATTG GCGGCTAANK GCAANYXGG	420
GCTTGTGNTK TTGCGXGGGT CGMAATTTG CACCGCGT TCTTTCGATA CGAAACGCG	480
CTGGGGCWCC AGMCGCGAA AAAGGATAAT RAAGAGGTC CATNCCCAA ACCGCGGCG	540
CCGAAATTCG ATCCGTTNCC MBCGCGCGCA CGCGTAAACK TKGCGAAYTTT CTGMAACCCC	600
CGAAGCCCGA TAACTTCGR GAAGGAGCTC CTTCGCGGG GCGNNNCRAA ACASCGTTAT	660
TTCGTTTCTT CGGCGCGT CGGCGGAAAGA YCCGAAASTA CTTTTTCGGT CGAGAAAAA	720
ACCCGCGCGC CGCCCGSNAA WTTATTTTCTT CGCGGAGCG CGAAACCTT TCAGAGCCK	780
ATTTTGTCTT CGCTTSCAT TGGCGGRT NCCTNCTTY TAAAAGKESG CAKWSNNGNG	840
CGRNNAOMA ACCCGAATG CTGAAAAATG CGCGCGCGT CGACACGNG TTGTCGCGAA	900
ASCCCGCGCC CGCGCGCGAA AACCGGCGCGA RKANTCGCGA AAAACGNYNG CGCCCGCGTT	960
CGAAAGGAAAG AGCGCGCGCG RMAAGGGGGN MMCCCGCGKA KTTTTTCTTT TCGCMRSDDC	1020
AAAGCAGNRY KGCTTAAAGAA CGAAGCAGCG TCCGAGANNN TCGCTTWSN CGCGCGCGNA	1080
CGAGSGCGCGC CG	1090

## (3) INFORMATION FOR SEQ ID NO:324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGCGNN NAGCATCTT CYGTCYACCG CGGTTCTAKT CGCGCGCGCG AATCTNGCTCA	60
AGGAGTCTCTT NAGCTCGGGC ACAAAAGCTW GACGAGSYNT CGNGCNMTC GTCGTCCTTGA	120
TGCGAAAAAGC NGTACGACAC ASACGCTAT GTCGTCGCGC GACGAAATGK TTGGGAGTC	180
GCTAACCGGT TGCGTAAACG CGACGTTGCG CTCCTTACG GACGAGTCG AGCGCGCGCG	240

ATATTCGAGG CACCAACCCCC AGTTTGTGG ACAATGCCCTT GGCATTTTCG TCAAATTTTG	300
TGAAACCGAA TTGCGMTTGA ACCCGCCLAGS CCCTCENCCNR AACATTTGGG WTCCCCTTTT	350
CTCCCCCGCC KTTTCCCGGGG GTTTCGCGAN RANCACACCC WTGGTTTCCTM TCNCGGCGCC	400
GGCGGAGAA NTGGGTTGC AATTTTGCGA ATGGGSSCCS GGATTCGCSA AACGGGTTGG	450
GAAACTTGTG YCRAAMACCC CGAATTCGAA TTTTCCGGGCE ANRAATTTCTN YCNACACTT	500
GTCTTACTT CGCGGACCGT AACMATTTC ATCGCTCTTNN CCTTTCGCTT TGCGGCGGGG	550
CGAAAYACCG CTTCGGTTT CGCGGACCGTGC CGCCGAANTC CGAACCGCTCA CTTCGATTT	600
GGNTCGAATT CGCCCGGGT RANACCGCC NTGGCCNNTT CGGASSAAAAA NGGGCCCTNT	650
KGGCNSSCCC AGTAANACCC TACCGNNTTS CANTCTTGC CGAATTTGG ACCAANSNTG	700
GGTTTCCGGT ATTTTGTGCG GCGCGGCTT TATGGGSGTTT GCGGCGCTTC NCSTTGGCA	750
MASSKAYCCS NGNGGGGT ACCCGGTTTG CGGGGTTTTT NGGGGGCCCCC AWAYGNKSTG	800
GGCCCGGGG GGAATAATWT NTGGGCGGG CGGAATTTT NTGGGCGMC CGGACTCCCR	850
GGGGGTTTTT TCGCCGCSA NNGANGGGG CGCGGAAATT NTGGGCGGGG KNTTTTATTT	900
TTTGGGCTT TCGCGGGG CGGGGAGAAA ANAAGAAAAA NAKGGYKNTT	950
TCNCACACTT GKGTTWANK NAGAGKTCCT CGCGGCGCG SNTTGTGTTT NGNGGGYGGG	1000
GGNGGNNAAA AGKNSRNMAC KGSTTYCCCG CGCGGCGCTCG NGNGGGYGG NGSCGNTTIN	1050
GGNGKRNNTA TNGNGCGTT SCCTCGCCCG CGCGGCGTGTG TWTGCGMYGG C	1100
	1151

## (2) INFORMATION FOR SEQ ID NO:325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AYTTCGGCAC MNGATTCAC GAAKCTGTGT CGCCCGACAA AGTGGAGCTA TTACTACTG	50
TATGTCATTC TCAACATTT CTGCGCGTAC KTGCGCGGTG CGATGCGGGC CGCGGCGTAK	100
TCAAAGGTGT TGGCGCGAGS GCTATCGCG CGAACCTTGC CGGCCCGCGAC ATCAKCGCCG	150
AACGCGTGCAC CTGCGCGCCG ACCGGGGTC GCGAATAACT CGAAACCGGT CGCGTGGTG	200
CTGGCGACG CGGTGTCCG ANTCAACTC AGCGCGCGMA CGAAGAACAA NAACTTTGT	250
CTGAAAGCTCA GTTCAAAAG CGCGGCGTGC CGGGCGCGTT CGCGGAACTG TNGGACTCKA	300
TCGCGGGCG CGGGGCGMC CGCGGCGTGT TGTGCGGTT CGCGGCGCCN AAAGCGAGCA	350
TCGCGGGCG CGCGGCGCCG CGCGGCGAAS TTGCGTACCG CGCGGCGCGAT CGAATTGCGC	400
GGGAACCGGSN CGCGGCGTGC CGAAGGGCC CGCGGCGCGTGC CGCGGCGCGTGC ATCGCTTGTG	450
NAAACGCGCGA CGCGGCGTGT CGCGGCGTGC NGNGGGGAA CGCGGCGCGTGC CGCGGCGCGA	500
TTGGCGGGCG CGGGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	550
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	600
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	650
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	700
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	750
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	800
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	850
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	900
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	950
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	1000
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	1050
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	1100
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	1150
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	1200
CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC CGCGGCGCGTGC	1250

## (2) INFORMATION FOR SEQ ID NO:326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GGGNTATAACA TGTCTGTGTYA CCGTACGGATCW ANTGCCTCCCG MAAXCTWSTM CASAGATCTC	60
AAAYTCTGCA CGAASCAGGCAGC AKAAYSTCGT COMBACCCCGT CAYTACWCCWG CNGCCTCCWT	120
CTTTEGACCGG GCGATASMC ACCTGTTGCCG CCGGCGCGCA CCTACACCCAC CCAGCGCGCC	180
AGCCGCCCCCN TEAMCAAACC ACCCCCGCTT TACCGCCCGC AGCGCGCGCG CGAACGACCGG	240
CCCCAACCCCCC ACCAACCGCG CGCGCGTTGC CAAAACCGCC CGCGCTTTTC CACCTTA	296

(3) INFORMATION FOR SEQ ID NO:327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NGNGSGNNNY ATCATCTTTC TGCACCCGGG MTCWATTGCG GCGGCAATCTT TSTMNSASAGA	60
TCTCGAAATTG CGCGAGARCA TCTGGCGCGSN SAATGTCCRA ANGSTONKTAAC CGGOMATOGG	120
TTTGCCGYCA ACTACKCTRT SCAKATGGG CGCAMWTYCA AACRATTRAT TTGGGYCCAG	180
AAAATTTCGG CTGTGRASCA ACCTGCGCGG GGTGRASCAA CAGGCTCTTAA ACCGTTAAATY	240
GTTAGGTTNT YCGCGCAACA AGCTGTATTA TCGGCGCGCG AMCCACAAAA CCTGNTNTGT	300
TNTGNCRAA NCCTGTYCCG GRAGGGTGTAA ACTTGCCTTA GGTGTTTCYC NCCTTRACAT	360
TAACCCCGCC CGGTCTWTCG CGCGCGCGA ATYCTTTCG WTGGTACCA CGCGCGCGT	420
CGTATCGTC PIAACGATTCG CGRAAGYTM MCCSTLCCCG TGGCTGATYC KTGCGTTTCG	480
SNAATTGCGG GATTTACCGG CGCGCTTAAV CGAGGCGCGG TTTGCTCYK CNCLACCGS	540
ATCMMCCGCS TACTTCTTAA RATTCTTGTG GGTGGAAACCG ANYTCAAAGAA NMNTTTCGCG	600
TCTAAGGGCGG CGCGGAATK CGACHTGGTK WACCGCTTNC TTGTAASSTT TCTTOMCGCG	660
CGCCCGXAAAS ANACCGAAGC CGCGGAAVYC WTGGCTTGTG TGCCCCSTTA AATTCGTCYC	720
AATCCCGCGA CGCTCGCGG GGTGSSCCONT TAAATTTGT CGCGCGCGCG GATTCGTCG	780
CGNGTMATTW CGCCCGTTTT CGYGTGKLAAC CGCCCGCGCG GGTGTCGGCG NTTSSECCG	840
GTTGSAATYC AAAAATNGGG MNCCTGAGNC CGNACCGCGH GKGCGGATW TKAAYTCYGG	900
CGCGGTGTCG CGCGCGCGAA AGCGGTGCGC KGCGGCGCGT CGMARTTTTT CGCGCGCGAA	960
ACCGGGCGG CGCGCGCGCG NCGCGTCCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	1020
MTCGSNGGG WTGGCTXNRTC NGCGCGCGCG CGCGCGCGCG CGCGCGCGCG ANC	1073

(3) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGCCCCCGTC	TTCCTTTCAY	TCTTTTCCCG	GGCTCTAGTG	GGGGCGCGAAK	CTTGTCTCRAA	60
GATCTGAAAY	TGCGCAGAS	ACGATSTCGG	GTGCGGCAAT	GTGCGGTTGG	SCAACATTTCG	120
GCTGGGAAAT	YGGGGTTAA	CGCGCGGTT	RATGGGTSTG	GGTATATATCG	GGTTGGTAA	180
TGCCCGAACG	TACAAATTTCG	GTGTTGCGAA	ATATGGTGTGT	GGGCAATATTC	GGGTTGCGCTA	240
ACACCGCGAC	TTGAAATTTC	GGTATTSGGT	MACCGGTRAY	AAYCTGCGCG	GGTTCGCGTGG	300
TTTCATACCC	GGTAAACGGGA	ATGTCGGTTT	YYYACYYCGS	SSAACGGNNW	TTTGTGTCCT	360
TGAGCGCTTGG	CCTGAAAMTSM	KGTTGTTTGT	MTYCGNGGAS	TANTTINMCCC	CCGAGTCKSC	420
WAGCCCTCGT	CTTCGCGCGC	GGGGTGTCA	MNCCCGGTTG	NGYYCCCTCC	MINTCYCAYT	480
CGATCCCGGTW	CGCTTINMNCG	CSCMCYCTTC	AMGCGTASGX	CACCGATTCG	CSACKGCTCT	540
MCYMCSCAGH	WTTCGCGCTT	CGTTTINCCA	MCMCSCGTCM	TGTAACCTCCEC	CGGGYCXNC	600
WYCTCTCXCP	AYTMMAACXX	TYCTCNCWYC	TKYCKCKKAG	WTTCGCGCTT	ACTCTMINTT	660
TCTCTCGGCC	OMGACCGTTT	CTTNCACCCG	CCACAKAYMC	TAACMTWTCG	MCTGACACCC	720
CTTCGNTTCM	WWCWCNTCNC	TWNAXCANCN	TTCTTCCTTC	WMMYTMKACCG	WCRNTCNCCX	780
SGACCTTCTC	ACTSMKCCCG	TCCTCTTMCX	CCYMCNCCTCG	WRYNCGCTCG	WMTGTCGKTT	840
GCTCGCGMY	CTTANCAAC	WMCCTCCG	WMCCTCCG	WMTGTCGKTT	WMTGTCGKTT	900
GCTCGCTTAC	WTCTTCGTCY	WMCCTCCG	WMCCTCCG	WMCCTCCG	WMCCTCCG	960
GCACGCTTCT	CTTCGCTCNC	ACCTTCGCK	CTMCCTCNYC	WRCCTTCGTT	WRCCTTCGTT	1020
CGTGCCTGCTM	CTTCGCTCNC	TCCCGCCCAT	CTMCCTCNYC	WRCCTTCGTT	WRCCTTCGTT	1080
KGTTTCGCGTG	CTTCGCTCNC	WCGCGTATC	TCTMCCTCNYC	WRCCTTCGAC	WWTGTCGTT	1140
ACTCTCTCWW	CGCCCGCGCG	WTCTCG				1166

(e) INFORMATION FOR SEQ ID NO: 122

#### (ii) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(xx) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

NGGCGGNNRRT	CNTACATCWN	TCTTCACCSG	NGMTCTTATTG	CCGCCCTCAAW	NETTTTGTGAS	60
AGAATTCTCN	AAYTCGGGAC	ANATUTTCTTY	TETTTTAKTGT	CCUCCTTGCG	CMCCGCTTAT	120
STGYGACTG	GTTAACCCGA	CCCCGGCSGS	CGGGGCRACC	ACGGGCGGAA	TSCAGGGCCC	180
GGCGGGCGCG	GGGTTTATAT	RAAGCGCGY	TTTTTCTRATA	ACGGTSCCGC	CCCGGGGTTA	240
TTACCGGCAA	AAYCGGAAKTT	TTGGGTTTAT	AACGTTAATT	GCACCCGGTT	TTTTTCGGGTG	300
AAAAAACTCGG	CGGGCGGAAAC	CGGGGCTCT	RAAGGGGCGTT	YMCCTCCAAA	WTNTGGGCCC	360
AAAACCCGGT	TCTTATTTTN	TTGGTTATSC	CGTTGCTTGC	GCACACGTT	CCGGGGTTAA	420
TCCTCTTCTG	GGGGGGGGCG	AAAACCCACC	AATYCGGTTG	CGGTGTCG	CGACGGGCGT	480
TCCTTCGNSY	CACTTGCGCA	AAYYCCGANT	AAATTTGGGTG	CTCYCTTSGS	TTGTTGCGCY	540
CATTTACCT	CGGGGGNAAA	GRRAAAANAA	ATCTTCGTTT	TGCTCGTCA	YCTTTMTTGG	600
SRAAAGGGGT	ATGGCSCGGT	TTTTTACCT	CAAYCCCCNA	NCATTTACCT	TTCCGCGCGG	660
GGGNNNAA	CGGTTTNGCTG	CGGGGNRACC	TKTTCMCCG	ATCNAAGGC	CGGAAATTGG	720
TVVSSTTCNA	ATTWTTWKKY	CCCCNCTTGC	YAAAAAKCCA	AAASAKCGGK	YCNCAAGTET	780
NGGGGTTTSSG	GCCKNYCTT	SNMTTAACCG	CYCCUCCAAAA	YVNSGGGGKT	TCCGCTINSAT	840
KGCACTTCCG	GGGGGGGCGNA	SAAAAAAAY	TTTYCCSARA	ATCUGLCTY	TCTTETESTRY	900
ANACCCCTT	TTYMKKRYTC	CKYSCNATTG	SGMTTCWAAA	TYCCGGGGGT	TNTTCCCCGK	960
CGGGGGGCCCC	AANTTTCTTT	YKNANNTTTC	CGGNRANNCN	AWTMGGGGKS	KCCTTCTGGE	1020
SCYTMAANT	AAANAAANGG	SKTTTTTCTY	MNAAACACGN	GTGKCNINCN	CNAAMBAASN	1080
AKDAAASAGN	KKKMTTNNNSA	AANCCGCCCC	CTTSTTINYTT	NETINONCSCC	CTGGGGKEDGM	1140
SWSWTTTTCT	NGCCRCGCCCC	YNTTNTGANA	AAUWNCYCCE	GGSTTMCRNAN	ASWMTTTICK	1200
GTSTTNGGCC	NGMELNNANAN	MCAMWNYCCE				1260

## (2) INFORMATION FOR SEQ ID NO:330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NCNNNNNNNA	TNAYAYWYCT	ACSSGGTCTTA	TCCCCGCGW	CINGTMAASA	GATCTGNRAY	60
TCGGGAAANAN	GCNTMTCTMC	CATATATAAAC	CATTGGCTCS	GWTGCLMCT	CAAAGCTGTC	120
CTTTCGKGCCG	TTTCTACRAAG	GTGSGMTGTT	CWYCCCTRAA	SCCTCTAIC	TTCTKTATYC	180
CTTGGGCTTC	ACTTTTACGS	SATKSCCTGCC	TTTCTAYCATT	RATGCRANTA	WTGGCTCAWT	240
TTTGGLAGGCC	RACCGGCTCT	TTTYCCGCGA	GRACIATNGA	TTGGGANTCGG	TYCGCRAAGCC	300
CCCGCACGAR	ACCGGCGGCC	AAAGGTGCGC	GCLAWTSCCT	GGTGTGAAA	TGTGCAAAC	360
AAAMCGTTC	CGGGTTERC	CGAGGTTAMC	ACAAKAAART	TCCGWTGGCC	GCACCAWNT	420
TTYCRATCNY	CWYCCCTCAGC	TTRAATTTK	YTTSCTGATT	GCCTTCCTGC	CTCBACAGCN	480
YCNCCCTCA	AACTCGCGCT	QACTCCAACT	GCTCTGGCG	AASGGGGGTT	CAMOGACAA	540
AACTCTTANN	TCGCCCATT	TCGCCCCCCC	CYCGGAAAM	GKTGAATMTC	TCSNAACCGA	600
CHGGGTTTV	AAACCTGAA	CGSSGENKOA	MYNSCCCGGA	ANTTTTCT	TYNDGGCGRN	660
AAANCGTTTT	AGGTTACGCC	KGGNGGGGG	CGCTTTGGG	AAAACAACCT	CGATTGCTT	720
TGGALLATTT	TCNCGCCCA	TTCTISGGGG	GGGCGXAMC	CGTCCTTTIN	TCMSNNNTYY	780
YCTTGGGAT	TTYTCCGCGCG	GAAYTCGGEM	CGCGYCTTRA	NCOCOMWNGG	GETYSTGSHAR	840
GGRATMWWI	TYSTTTVYMC	CCCGCGNNCC	CCCTAALMNT	KENTGALCMA	AAAXCSCGGG	900
GGCTNNNTY	YCNNNNNNIT	TCRGGGTTNT	TYMAAATSA	GGGGNNNTY	CECCNGSOMN	960
GTYSGGGCT	TTTCCNTTTC	GGGGATYNG	MACCCCTTNT	AYCGGGGGGT	WTXTXCCCC	1020
SC						1022

## (2) INFORMATION FOR SEQ ID NO:331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:331:

NNCCNNNTTA	TNAYAYWYCT	NCACCGNNNA	TCAWATTGCGG	CGCGAAATCTT	CTMAASAGAT	60
CTKAAYTCG	CGAMGACCG	CANCTTATTG	KGTGRASCGC	ACCGCGCGA	CCTYNGCGXT	120
CTTTCCTTGC	AGRGAGGGCC	TGGGTGGCRC	CGCTGGCAT	GCCTAACCGCC	CCCCAAACCN	180
CGCGAAATWT	CTAAAAACAA	CGCGGGGTTA	GKTCCGGGGCC	GCCTAAATMAA	TAACCTTCTT	240
AAACKAGGCG	ACGGCGAAC	GGYCCCGCC	AACCAAGGNA	CTTCCCCCSCC	NATACTYCCG	300
GTGGGGCTG	CGCTATYCC	AASTGCTCA	CTCNACGGGM	CGGYCOMWNT	TCCGCTTCT	360
CGTGTCTCG	TTMMATTTTC	CTTCCTCYTG	CGGGGIAAC	TTTTTTCYCN	CTTTCGMA	420
CACNNAGGT	CTAAAATTC	CGTTCCTCTG	SNNCAAAYGR	GATTGGGTT	CGCTTTTTNT	480
TCMCCOMAAC	CGCTTTTNA	CGCGGMMTC	CGTWTAC	CGCWNMCNNE	ANXKTTGNEA	540
AAKTNNEZCC	RAATTCAAA	NTTTCGGCGC	NTTTMTWMCY	YVCGTTTCCG	CMCCCGAAA	600
CGCTTCTTY	TUGGGAAATY	TCCCTGCAA	ANTCAGWCG	TTTCGCGCCA	AGAANTTCSC	660

SACTTCTTTT	TTTGGGGGAA	AATANATTYYTT	YCTTNGGGSK	TTCGCGTCCC	ANMAATNTCC	720
RGCGKAMGCC	AGCTTINNTCC	TTTCCCCAA	NETTYCCYKGS	RMCYTNFTCY	TTRAANFASR	780
SAACCCCGGS	GKCTINCHCS	TTACCCCCAM	KAAAATTTCG	CCCGSSETTC	TTYNINKEN	840
GGCCCGGAAAM	ACTTNTWATT	TTTCCCCGNN	TTTYYCCKCS	KCAGMMNNTTG	EECNCTTTTT	900
YCSCMATAKA	CTTNGGGCCT	NTCTTGGGGG	QHAAAMAAGG	CCCGSSTTC	TTCCMMNAGA	960
TTTGTGMMKA	SAAKAKWATA	AWWNTTRKYE	TINMCCCHCC	CCRKCTTISNN	TKXCONKES	1020
GGGGSWWKEE	GWCTTGNCGNC	CKCCCGCKNK	CCTWATTAACC	CCCCSKKCCG	KGMDNTTTC	1080
CCC						1083

(2) INFORMATION FOR SEQ ID NO:332:

## 1.1 SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1069 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### (iii) MOLECULAR TYPE: Genomic DNA

(xii) SEQUENCE DESCRIPTION: SEQ ID NO: 133.

GGGGNNNNYAT	MCAYCNTOTG	YACSGGNGTC	TATTCGGGCC	CCMNYTINNM	GASAGATCTC	69
GAATTCTCGA	MGAAAAAAAGW	GTATUTCTTG	ACCTTMCGGC	CCGGGAACCR	ACCEACAAAAG	120
RAASCSCGCT	ANAAATATTGG	CCACRNTTGG	TGACATATTT	ACCCCAATTNT	AYCAGGGAYT	180
WCACATTCCG	GGACCRACCG	CCACATCCG	ATTTTNTTTT	GCRAACCTTR	ACCTTCCCGA	240
MTTYVGGCRA	STTGAACCAG	GGCRAAAAAA	CGGCCHAAWY	CTONKCTTGA	NTCCCGCTC9	300
GGCGNAATAA	CTAGGCCCCAT	TRAACCGAAC	CGGNGGCCSC	KNNTTGGCA	ACAGGTTCTR	360
ACLAAGGGCC	CCGASTYCCG	CCGGNTCCCG	TTTCACNCCC	TNTCTCTTG	CGGAAATYCGG	420
WTGCAATNYC	CNTGGGGCCT	TTTCACTTCG	KGCGGTTNCCA	ANTCTTGGTA	TNTCTATRNG	480
TCGCGTAAAT	SCAMANCTGG	GGTCGATT	WTGCGSNTTC	KATTTTANNN	BRNGCGTTCT	540
TCAGTTTCTRA	ARCCGNTTGG	GGCGNNDDCA	AAAAATGATN	ATTAATRATGN	YGSCSTTCAA	600
ACGTTTGTTC	CGTATTCGNT	GGGTTTGCNC	CGGGCNGGT	TRAGKTGGA	ATTTTYTNMTC	660
YDNASCCCT	WATTTTGGNA	AAAATCTTC	GGGTTCTCAA	CTTTTTTTT	GGKSNTCGG	720
GTATTTTCCG	CGAAACCCAA	ATTTTNTGG	GGCYCGTNAA	ACGCGCTTC	RCOGGAATT	780
TTTTTGGTTC	AACCTTAACT	TTTTTAAACC	NTTTTTTTT	TCGCGSCMN	TNGSSCGENT	840
KSSCCTTCTT	RANKKCTTNN	GGGGGTYCTN	GGGCGMMTTT	CTTTTTTTT	CGCTNNMAM	900
WGGTTTCTCA	AAGMGGCCCC	GGCGGNSAA	ACCCGTTWAS	TTTTTGNNA	AAAGWYHNGN	960
KGCTTCCCGG	MMNRAAAAAY	GGCGGNSAA	GGGGGTTWAS	TTTTTGNNA	AAAGWYHNGN	1020
TYCGNGSYCCG	CGMAYSTYT	YCGGCGGRR	ACGSMNGGGA	CCCCCCCCSN	HTTRKTTTTT	1080
TCAGANAKNEE	GAMMSKTTT	TTNNGCGNNK				1140

(2) INFORMATION FOR SEQ ID NO: 1

#### SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1010 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Gennomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

WCGGGGGKWL	MACACATCWT	TOTTCAGCG	GCATCWATTC	CGCGCCCGAC	TCTTGTTGAA	600
SASATCCTGA	TTTGGGGCAM	MACCGACCGC	TCCTAAAAAA	ACCCCAACTT	CGGGSKOTYC	1200
CAGLACTGTT	CCCCATTTTA	AACTTAAA	ATTCTGTTTC	ATCTCTTCTC	GGCGTTTCTT	1800

YCCCCGGCGAA	GGGGCCGCGA	CCTGGAGAGA	SCATCCTATG	GTCGTGTTGATG	CGGGGGGGG	240
CCGGGTAAAG	GGACTTGCGT	GGTTTGCSC	TMCAAANATC	WYCCCGGGGT	YGTGTGGAT	300
MNCNAGGGGT	GTCAAAAC	GGCAACAGCG	CAACCCANCG	NTTACGGGG	CTTAAANGA	360
AAAAGGGCTG	ATGCCCGCAA	GGGGGGCGGC	NCCTAACCTT	CGTTGGTCA	ACRACCGGT	420
CTCTCTGCT	RAATTCGENT	CCRATTCYNG	CTGGGTTTC	TYKTCCTYCT	CGTACCCGA	480
ATCTGGGTAT	CTTATASTGT	CCCTTAATWT	CCAAATCTTG	GTTTGTGAT	TECTTTSCTT	540
TCCAAATTAA	CTMCACACCG	TTTCTTNGAT	NCCTAAACCG	GTTGGCGCC	NRACCCGAA	600
AAATGAATTA	TAATAANNGG	KNNNTTTCNA	ACCCCCCCCC	CCCNATTCGA	TYENNTTCCA	660
NMNCOCOCAG	NGGETAGOTX	GGGAAUANTYC	TCMACCTYCA	ANCCCTWARS	TTTTTGAAT	720
KAACCCCTT	YONGGGTCWW	TYMALLAAMA	NTTATTGUGG	NGNTTTGGG	MNNTTGTGST	780
SCCAAAATCC	MAAATANTTT	YTGGTTCNA	TXAAAAMCG	YONCKCMGCC	GGAAAATTTT	840
TTNTGTTSA	ACCCAAAAAC	YTTTTOMNAA	NCSSKTTTY	CTTTCCCCCC	ASNTGCGYS	900
GGGNATGTYG	SCTTTCTTA	TEPEYTYMTW	CMGGGGGGNN	MNNTCTMCCC	COMTTTYYCY	960
NNWETTTTIN	ECOCCKTME	NTTAANNGG	YTCSYNAMAA	AANNNNNNC	SCCNCTTNA	1020
AAAANCCCH	NRNARAKTNT	TTMEANNTNN	SKCKNKGKTY	YCCCCCCCC	YNNNNIAAAA	1080
AATMYCCNCC	RAGANMCASH	NNGGRGNRSC	GGGGCCCTTT	MNNTTMINTT	TTTTTCCSA	1140
GAGCNCCSCG	MEGANMGNC	CTTTTFCND	NGGNKNGNN	GGNGRNKKG	CCNAGAANWK	1200
CTKSTGCCB						1210

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGGSSNOMNA	TMCATCWTCT	GYACSGGGMT	GNATTGCGGC	CGGACTCTNT	NAASHGATCT	60
CGGATTCGTC	AAKANACGCG	ACCGCCGCTGT	NTTAACTCGG	CAAACTTTCT	GTXTGCGAA	120
ACCGGAGATC	GGCGGCGTG	GGGXYCCALC	GTCTTACIYT	ACCCGCGATY	TCATGTTRA	180
ACCGGGTGT	ZAGGGCGCGA	ACCRACNTAA	ACGCTTTAIC	CAAGGNTTC	GTGGGGGGC	240
ACGGGATCTY	TUTGGTGTGT	GTGNYCGGTG	GTAGGGGGG	TTAANCCTTG	TTGCGCCTY	300
AMCAGCSCGCG	CGGTRATTCG	AKCNWTCGCC	CGGNNRACG	CAACGGGCG	TTTGRACGGT	360
GGGGCCNATT	CAAAYCXCT	GRNTGCTTOM	AAACRACCAK	AAACGGAATM	CCNSCACNA	420
ATMGGRANT	TTAAGGCGC	GGCAAAACCT	NTRAKNCCT	CCGGGCGAA	GTCTCCSCAA	480
SCCATCCTAA	AAIACGCTAT	TTCTCCTAC	ACRACCGAA	NGCGTTTGC	TTCTTCGGA	540
TTGAGAMCA	ATTMNGGEGT	NTCTNGGAA	ACACSCINCC	NTTAACTGNG	CCCMCGGGCA	600
ATTTGCGRAA	SAACCCCTNY	CCCGGTTTIT	YGTGTGOMG	CCCGGAAAC	CTGGGGGATC	660
AAAASAGTTC	GGNCAALANG	SACCGGACTT	NTTCCCTTTC	GGGGGGCGNN	CGGGGGGAA	720
CGGGGGTAA	ANWSCTCTTT	CTSGGCGAA	YGGGKCMAAA	NGKRCPTGGK	TTINGGNNAC	780
NTTTCGGGNG	CGGGGGKOKIE	NGKCYCTNNA	CTTTTNTTTT	SCCGCTYQAA	NYSGCCCGGG	840
CGGGGGCCCG	CGGGGGGGGA	NTTTTNTNA	GTGTYCCCT	CCCGNAAA	ANACCCCNYC	900
CGGGGGGCGT	TTTNAAATM	GTGACCGG	GNNGGGGKCM	GGTTTATTTT	NNNGCCCGGG	960
TCGGGGGAAA	AAATACTTTT	SYCCCCCGNC	CTCGGCGXGN	GAUMSMECSC	TTGGYCTCNC	1020
CGGNTTAAAN	ARSNCXCGN	CGCTYKCGGS	NSNGKCNWCD	NGCSTTENCT	NGGNCNKN	1080
XAAAAGAATYC	NGSMSTSSWV	CTKCC				1140

## (2) INFORMATION FOR SEQ ID NO:335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 916 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(II) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGENENENNN	TATAYCWTYC	TSCACSENGGA	ACWANTGGCGG	CCTRMAMCTNS	TMKASAGATE	60
TWGAAYTCGT	CAAGAGCCGC	AGAGACTGTST	GCTCTGTTTC	ANAGTSTMNA	CCCGGTGCGG	120
CSCGCTGKTR	GASCACMCT	WTGCGRACAC	CAAAACCTTC	GGGGGYCNC	GGCTTGCGT	180
GCALAWYCT	CCGGGCCAC	TCAACAAYW	YCTVCTUGAA	CCGARGCCGT	TYCGCGCGG	240
RATCUTDGET	CASYTCGGCG	TGCGTGTCCC	AAGCTACTCG	CCAYCMAAA	CCSCTCCCG	300
RAACTAACGT	AAWTTTGCCG	AAATTCTTC	CCCTCGCCG	TCATTAATT	NTWAAGCCAC	360
CCCAAMCCTY	CGGCGCTTC	CTTCTGCCA	ATYCGWTCG	RATAYCGCG	GGGCTTAKTC	420
KYCTCYKTC	GTACCGAAT	CTTGTGTTTC	CTATATNTYC	CCWAARNECA	ANTCTGGCK	480
KTCGATNTSC	TGCGTTCGA	ATTIAMAACA	NCGGTTTCTT	TWTACCAA	AACGNTGCG	540
CCCTTACCGA	AAAAGATNA	TATTAAGCTG	CCWCAAAAC	CGGGCCCCC	RTTTCGAYCG	600
STCCACRGCG	CCANGNGGTT	AGGTTGGAA	TYTMACCCG	CGGGCTAA	GTINNSGMA	660
AAACCCCCCG	GGWNYCRAA	ASMTTTTTG	GGGTTTSGG	CTATGTYKOC	AAAACCAA	720
TWTTTCYGYT	CTNAAAAACC	GGCCINTCGS	NSAATTTTTT	CGGAACTCCA	AACCTTMM	780
CCWNTTCTY	YCCONEACAA	TGGCGGENTG	NGSSONTTTT	TWTTTYNNA	GGGGGHERNC	840
SNCCCCNAAN	YTCWMAAING	NGCCCGGMA	AAAGAGANIT	YONKAALLAC	CCCONCNCC	900
NAAAATACCCC	MKAATNTTCM	AAASMSCTNG	YCCDDC			936

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(II) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NNNNNNNN	ATMMAYTCWY	YCTSCACCG	GGGTCRATT	GGGGCCRN	WTITGTMAS	60
AGATCTTNA	TCGGCGACAG	ASSESCACAG	ASCCCGCGCG	CTATYCMICC	CTTCTCTCATC	120
CTGAGACCG	TCCTCGGCG	GRATAATGGC	NGGCGCGCG	CCCAACACCG	YTCAAYTGT	180
TGAGAGACG	CATATTCRA	CAAGGTRATA	AAASCAAAC	CCGCGCGG	GGGTTGGGC	240
SCGCGAASCG	GTGCGAACCG	RAAACNCCTT	GGGCKCYCGG	KTGACTTIA	AASGGTAAATC	300
TCTCTCTCT	GGCTATCTGT	CCGGCACARA	CCTTGTGCGG	WGGGTCTCG	CTTGGGTYCNC	360
CGTCGCGTT	TAINTTCGCK	YTCACACNT	TKGGTYCAG	CAACCGMTT	CAWAAATTG	420
TTTGGGTTG	GGGSSCGCG	YTGTTCGCG	TAATAATCG	NGGTGCGCG	MYCAGCCGWA	480
CCATANCGTG	CCCGGCGCTG	CGAAATTTC	AAAATCTTT	CCTTCTGTCAC	CCWACAMRC	540
CTINEAAATCC	GRATCAATNC	CGCGKGCGCTT	NTCYCTCTCN	GTGGCGG	TGTTTCTAT	600
RTINCGCYAA	TSCAATTGCG	TTTCGTTTSC	YGETTCCAA	TTWCAAMAG	GTGTTTCTMT	660
ACCAAAACCT	NTGCGCCNNA	CTNAAAAXNA	RAAAANAKOS	WTITTYLAC	CCCGCGCTTAT	720
TCATYGTGTT	CTENWCCCCG	NGKLAGGECH	GAAYTTTAA	CCCAACCGMT	ARSTTSNAX	780
AAACCGTTCG	GGGTENCAAA	MGTTWTTSSC	CTTCGEMCTT	YCAAAATMSA	AAATTTTCX	840
SKWNAAAAMC	YONCCCGSAA	ANATTTTTGT	NAAMCCIONA	YTTRTTTMC	WTTTTCYCC	900
CCTCCKNNSCG	GTTCGCGT	TYATTTCTG	MCNNNGAGC	CCCGTTT	WTWTCGTC	960
SNARGGSNNIT	RRGMNMNCC	CCCGCGNAK	NTCCONCAAL	WTITNAAGCN	NGTYCKCGCC	1020
CCCTWNNNN	CGCGCGT	TM				1042

## (2) INFORMATION FOR SEQ ID NO:337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GGCGGCGMXX	ATAMAGCTT	CTSYACCCNG	GNTCHATTGC	GGCCGMCNTC	TGTTTAASAG	60
ATCTCGAAYT	CGGCGAANAK	AGGCGAAGTC	AAGTGTTRAVY	CGGTCAACATA	TGTGCGGNG	120
TGCGACGCCRA	AGCGGNTCTA	CGGCTCCGCT	GGGGCGCCAC	GGCGATCGGT	RATGGAACYY	180
CGCGCGCGAC	GGYCGAAAGG	TCGTTTACGG	CGCTAAAGGT	CGMCATTC	TERGTTTMGN	240
CGACGTTT	GGGCGGCGTC	RANTVCTTAC	CTGCGATWTC	GGTAAATGGGR	AATTTGGGCR	300
YCGGTTTGGG	CAATAAGKTN	TTGGCGAACG	GCGRGNTTC	KGTCGCGRA	ATTCGCGCAT	360
TCCCTTACCG	GTGTCACGGT	TTTCCCGGTT	GGCGTAAATG	TTTCNTGGGC	GGCGTCCGCC	420
CGNNACASYY	CGCTAACGGY	CMCGACGCAA	TACCGTTGGC	TTTAAACCGC	CGCGATTAAY	480
TGTCACCGAC	YTCGAASETG	CTGCGATTC	TTCGCTGAA	AAAGCCACCG	AACCGCGGTY	540
RAYTGCGTC	MTCGACWTTT	SGCGGTTCT	GGCGTTTGR	AAVCTTNTAC	CGTYCAAAG	600
GTTCGTTTTC	CGAAGTAAATT	GGTTTTCGA	CGTTGCGGCG	GGCTGCGTTT	CGMCCTTER	660
AMTCGCGCGC	GGCGGCGAAN	ATTTGGGT	GGCGCGGTC	CGCGATAT	KGTCGCGCT	720
GHAAATTTGG	GGGATCGCG	GGCGWCGCG	CGWTGCGGK	TGCCCAGTTG	GGACRATTYC	780
WRCGCTTCGA	AACCGCGCGC	CGCGGCTG	GGCGWTTT	CGTTCGCGAA	AAAGGTTTGG	840
NYTTTTCGCG	CGAAGTTCGA	CGCGGTTT	GGCGATTAAC	TTTCGAACTC	CGACCTTTA	900
ASAGAATTCY	YCGTTCGCCC	TTTTTGCGCG	SANGCCCCM	NMSHGNCGG	AAAAAAAGNK	960
TYMCGTTTAN	CGCGGTTT	TTTTCGCGCG	WVWWSNMCY	NCWVWVWVY	NGENNNMCCT	1020
SKYEGCGATW	GGNNNNCGC	GGNCGMCNT	CGWNGGTTK	NGKXGNNCC	MSC	1073

## (2) INFORMATION FOR SEQ ID NO:338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GNNGNKNWTT	TMCAYCWYCT	CGCGCGGTC	TATTCGCGTC	CGAAATYTGCT	CGAGAGATCT	60
CGATTTGGC	AMNASHAATG	TGCTCGTCAA	TTTCGKGTC	CTCXTCAAAY	GGCGCGGGCG	120
GGGACCTTCA	CGCTGCGTC	CGCGAACANAC	GAACCGGTC	AAATWTCAG	GGCGATGCG	180
TRTCGAAATCC	CGASCAGTTA	ACCGTGTGCG	TGAAAGGTC	CGAACCGAGC	ACTCGGTTCA	240
CGCGCGCGCA	AMTCGCGCTG	CGCGGCTGTY	TCAGCTTGAT	TWTCGACCT	RTWTGTGCG	300
TGGCGAMENT	GGTGAAGGGC	CGWCGCGCGA	AGAAGTCAG	GGCGAACATTG	CGGGCGCGNA	360
GAFACTCGCG	GAACCGCGCG	TAGLACCGCG	CGAACCGAG	GGCGTGGCG	ATTCGATTA	420
NAMECGTTG	CGACNTGGCT	RAACGTTT	CTTGCGCGGC	CTCGGCAACG	CTGCGACANT	480
TACCGCGTC	CGCGGCGCGAC	CTCGGCTGCT	TEKYGCGAAAT	NTGCGCCCGC	GNRANTNGGC	540
CGAATTCCAG	GGCNCCANCT	TTGCGGCGT	AAATCCCGTC	CTTAATCACC	GGCGCGCGCT	600
GCTTTGGCGC	AAACGCGCYC	CTTGTGTTAA	CGTTCGCGCT	CAATGGGNC	STTGCGGAAAT	660

TCTTNTTCGGT	GGGGCGCGCC	AATTTTCTCT	TCCCCAASAG	CTTAAAGCCAN	TTTGCGGANTCC	720
CGGCGAAANS	NGGGGCGGAA	AAACGGCGCC	CGGNTCTCCT	GGGGXGGCC	CXGGKTTCAA	780
AATTTTCCGG	GTTSTTGCAG	TTTTCGCGCC	CGGCGAACRA	CGGCGTTTT	TTTTTGAAACC	840
KCAGTACCGA	AMCCGCCSSC	CTTCAAAAGGS	GCCTTAACGR	TAATTTCGCGC	CGAAACCGG	900
CCCGCAGTTC	GGGTTCGTC	CTTCCGGKGCT	CTTCTTTTMM	KAACCTTGTG	GGTTTTTAN	960
NGSCCTTTC	CACCCCTTCG	GGGCGCGRNA	GAATTTWTC	CGGGCGNNAN	ACCCCGCTTG	1020
GGCGCGCGCG	NGAGYSGCTT	CTKGCNQNON	YTTTTTCCC	C		1080

## (i) INFORMATION FOR SEQ ID NO:339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GGGGCGCGNN	ATMCAYCWTY	CTSCACCGCG	GMTCWATTGC	GGCCGCGANWY	TNGTNAASAG	60
ATCTCTGAAAT	CGGCGACAAAG	CGGCAACAGAG	TOTOTOCATC	TTTGTCAAG	CTGTCAACGC	120
GTGTCGCGSC	GTGGTGTGCG	CTCATTCUGR	ANACCGAAAC	CCCTCGCGCC	GYCACCGCGX	180
TCGGCTGCAA	AAYCCTTCCG	GGGACTTCTRA	AAACAAWYCT	CTTGTCAACSC	ARECGUTTYC	240
GGCGTGTGAT	CTTGGTGTGCG	YTNGTGTGCG	GGTGCCTCCA	GGTACTTGCG	CWYCRANACC	300
GCTYCGGSSA	ACCGAACGTA	AAITTTGCGW	AATTTGCGTT	CGCGCTTECC	TTTATTAATT	360
TGTTTAACCA	CGCAAACTY	CGGTTTCTTC	CTCKTGCGCA	WTCCGGRWTCC	RATNYCSCCA	420
TCGCGTTC	KGTCGTCYCG	GTGCCCCAAAT	CTTGGGATGT	TATATTGTCC	CTAAATGERA	480
ATCTTGCGTC	TCGTTTCTTC	GGCTTGTGAA	TTWAMNNNG	NGTTTTCTTY	CTTCCNAAC	540
CCGTTTGTG	AAACCGAAA	AAATGATWATA	ATATGTTGTC	TTTCAAACCC	CGENCCCRYY	600
GNATCGCGTC	AMNGCGTCG	GGTGTGKNGG	GTATTTCTPM	AAACCCGAAAC	CTAAASNTTG	660
SGAAGAACCTY	NGCNGGTYA	CTTAAACGUNY	TTTTTGGGTY	SSNTTGGGNN	YCATGGCTTN	720
CGTAAAGCTT	AAATCTTTCG	GGTGTGATAA	AAAMMMSGGTC	SAMCGCGGAA	WTTTTTTGN	780
KGTAAGCGAA	AAACCTTCTT	GTAAACGAA	WTNTCCGTC	RCRMMNTG	CNSGGARTKT	840
SSSGCTTGC	ATGKGCGAA	AGCNGGGAAGA	CGARCGGAA	TTTCTTNTIN	KGKGCCGIST	900
TGTAAGAAGG	GTNTVKGAA	AAASCYCCNC	NGCTGGCGAA	AAKANGGTY	AAAGAKNTCH	960
NAANAGSYSH	NGNGSCCGCCC	CTTGGT				996

## (i) INFORMATION FOR SEQ ID NO:340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGGGCGCGNN	ATMCAYCWT	GTTCGACCGN	GGGGCGCGAT	CTGGTGTGCG	60
GTGTCGCGAA	TTCCGCGAAAG	AAATGATCTCG	GGGGCGCGAT	TTTGTGTGCG	120
ACTTTGCGA	TCAACGATCG	GGGTGCGGCGA	AAAAAATCTT	ACCCCGATTC	180
ATGTCGCGTC	ATATTAACAC	CGGGCGGCGW	GGTGTGCGA	GGGTTGCGA	240
TCGCGTTC	TAATATCGAC	CGGGCGGCGW	GGTGTGCGA	GGGTTGCGA	300

ATMACCAGCT CCGCCAGGCG CACCTTCCCC AAAATTCCTCT GGTTCAGGCC AATTTCCCG  
 CGGGCCAAACM ACCAACCGCA TCTGGGTC AATTCACCG GCGCGGGGTG TAAAGGAGA  
 GATCTCTTC MANCCCGCAN TCAAGCTTAA CCGGACAGC CGCTCTTCCT CAGACCGCA  
 RTACCGGWT CAACCGCCS CTCAAACTCA ACAGGGGGNC AGGCTTCCCG CGGAGAAAG  
 GTTTTACSCC MMYAAKAAA MAAGCTCTT TTTCCTCCCTC CAAAGAAA AANCCCGCG  
 CGGGCCCTCN MMGGGGTTTG CGGAGAAAGA AARCCCGGC CGAACGAGTC CGAACAGTC  
 CAAAGTCCTT TWAAGACTCYN MMAGCCCGG ANTTTGGGA AAGGNTCCCG NTNTNGCCCG  
 TTTTATGCTG CGGAGMTCTY TAAAAAAATT CGGCGAAAAG CGGGGGGAAG GGTGAGCTG  
 CGNRAATTTC CAAMCGNNGK TTNTTYNGT TMGGGGGRA AATTCCTTC CGTMMNNGGG  
 CGSGSNRAT TNGGMSNMT TTINNAATIM EGKNTSAFT VNIKCOMNNN ENMMNSNKK  
 TNAMCXCCN CCTNGNGK YCSCYNGCCG CGAGGGGRAS MNCNANMAA AYASGTTTNG  
 CGGAAMMCNN AATTCNNMNC CGGAGSMNN NNMMAAATMT CNGKCNNSNN AAAGCNEACH  
 CCCNSNSGMN REGLAEMTNY TCCCCCGSMN CGCTAAAGAAG GKVCCCCCGM AARG  
360  
420  
480  
540  
600  
660  
720  
780  
840  
900  
960  
1020  
1074

## (2) INFORMATION FOR SEQ ID NO:341:

## (A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(B) MOLECULE TYPE: Genomic DNA

## (C) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NGNGNCNENT MTACATCTTT CTGACCCGCG GNTCAWANTCC GGGCGCANNK TTGTGAGAG  
 ATCTGAAAT CGGAGAGGAG ACWCTCGCGA CGCCCGCCCA NACTCTTCCG TGTGTACCCC  
 ATTGNGCGCK TCAGCGCCCG ATYTAATCAK TNGACTTNGG TGGCTTYYGC CGTGGCGGCG  
 GGCGTCAAGG CGTCSWCTCT RAAGGCTTNG CGCACCGCT TGCGTTTTCT RAACGCTTGG  
 AAAATGGCCG CGGTGTGGC TCAUTGGGNTC TACCGTACCC CGGCCCCCAA CGTTTUTTA  
 AATCCCGGTYCC WTGTGAGCC TTGTTGAAVCC CGGGGRRAGA ACTTGTTGCG CGCGAYTTG  
 TCGGACTTRK TCAAAATCCG CGAAAGTGTGTT TGTGAGCGC CGCCGGAAAGG NGAACCTACT  
 TTENGGWANG TGGGNCGCCG CGCGTATCA STCTGTATCA ACUGGGGAACG CGTNNNFTTG  
 KGGGAAAAAG RCGCTCAATG MTTGGTGGC GGTGCGKANC CGCGCCCTEK CGCGNAATG  
 GAAGGCAGAG CGTTAAGGCC MTTGTCGCCR RSCCGTSTG SGTNTTCCG CGGAKMAMN  
 NNMMANWTK TGTGGGCCW ATTCGCGGG CGTGTGAGA ANACTTCCW WCGTTTNTSC  
 GAAAGNTKCS CGCGTTTTC CGCTGAGAN TGTGATTTCA CGGGGGKTKCC CGCGGGTYC  
 CGAANWRTY CGTGGGGGMM CGTGGAGCCG CGMMATNAG AGMAGGGKTG TGTGTSNCC  
 TTGNGGACC WCGNCWEEAK ANAACTWKT TGGCGTNTG AGKNTWKGET YCGKTTTTC  
 TAAGAGGAAC TATGKCCCG CTKGAGCGM GAENGGCGG TGTCCCGKRT TGTGNGAAA  
 TATKSAAGGG TCGCGMAGNK CGCGTTTTCG TGTGAAAMN MSMRSGKXTC CGMEYTTSC  
 CGGNTTGTGA GAGTAKTCCG CGCGSMKAC WCGNGNGNG AGKNTTNTS YANTGAROY  
 NNNGKTMNT WCGCCGUNA GAGAGGCCCC CGAGMSTG YCGGKMSNG ARAGKATGG  
 CGGCGCGM CGCGGAGMGA SAGNGMCGM CGGCGKTGNC TCGCSCCGNS CGAGKELGAA  
 CGTGGGCGC CGCGGKTKT TTKTGTGATG YGTGNGSMNN NAGAAAAGAG AGCGC  
60  
120  
180  
240  
300  
360  
420  
480  
540  
600  
660  
720  
780  
840  
900  
960  
1020  
1080  
1140  
1185

## (2) INFORMATION FOR SEQ ID NO:342:

## (A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC CTTCGGTACCC ACCATCGCGG TCGGAACGAT CGCGTCATTC AGCATTTGCA 60  
 TGTTTTGTTG AAAAAAGGAACT ATGGCACTTC AGTCGCGTTG CGTTTGTTT ATGGCTTGA 120  
 TTTCGATTGCG AGTGTGATAT TTATCGGAG CAGCAGAGC CGACGCCCG GAGACGAGAC 180  
 TTATGCGGC CGCTAACAGC CGGATTTGCT GTGACCCAA TGGGACCGA TGCTCCACBC 240  
 CGACTCGGTG ACCGCTTTCA TGCGAGAAA TAATACCTTT GATGGGTGTC TGTCAGAGA 300  
 CATCAAGAA TAACGCCCGA ACATTAATTC AGGCAACCTTC CGACGAACTT CGATCTCTGT 360  
 CGATCGGG ATAGTTAATC ATGAGCCCGC TGACCGCTTG CGCAGAAAGA TTTCGACCG 420  
 CGCTTTACA CGCTTGGAC CGCTTGGTT CTACCGATGA CACCCACCG CGCGCACCC 480  
 CGTGGATGGC CGCGAGATTTA ATGGCGCGA CGATTTGCA CGCTCTTGC AGGGCGAGC 540  
 TGGAGGTTGC AACGGCAATC ACCGACGCT GTTTCGCTTG CGATTCGTTG CGCACCGGT 600  
 TGGGATGTA ATTGGCTCC CGCATCGTG GTTCCACCTT TCGCCCGTT TCGGCGAAA 660  
 CGTGCCTGC CGTGGTCACC AGCGGAGAAA CGGTGCTGATA AGAGAGCACCG CGATACCTTG 720  
 CGACATGTA TAACTTACT GTTTCGACAT TGACCGCTT GAATTGACTC TTTCGTTGC 780  
 GCTATATGC CATACCGCA AAGGTTTG CGCATCGAT CGTGGCGTG ATTTTGACG 840  
 TGGGATGTA CGGACTCTG GTTACGAG CAGCAGATA CGAGGTTGCG CGCTTGTACG 900  
 ACCGCGCG CGAGGAATGG TGTGCGAAG CGATGGCGC CGAACAGTC CGCGCGCG 960  
 CGGCGCGCA CGTACCGAC CGCGAACAA CGCTCTGTA CGCGAGAGT CGGAGCGCGA 1020  
 TGTGGCGAT CGGTGATGTC CGCGATATAG CGCCGAGCAA CGACACCTGT CGCGCGCGT 1080  
 ATGGCGCGCA CGATGCGTCC CGTTTGGCG ATGGAGATG CGATCCCGCG ALATTAATAC 1140  
 GACTCTAT AGGGGAATTC TGGGCGATA AGATTCGCG TGTAGAAATA ATTTTETTA 1200  
 ACTTITGAA CGGATGATAC AGATGGCTCA TCAATCATCAT CGTACGTTA TCGACATGT 1260  
 CGGACGCG CGGACATCTG CGGAGAGC CGCGCGCG CGCGCGCGC CGCGCGCGA 1320  
 TAGCTTGAT GACATCGCG TGTGGCTT CGTGGCGCG GACATCGCG CGGACGCGCG 1380  
 CGGAGAGTC AGTACCGCA TGTACGCGA AGTGTGCTTC AAGATGAGGC CGCGCGCGT 1440  
 CGGGCGCG CGAACGAGA CGCTTGT CGAACGGCG CGCGCGCG CGCGCGCGT 1500  
 GACTACCG CGCTGCTGC CGTACGTT CGGAGAGC CGTACGCG CGTGTGACCG 1560  
 CGTGGCGAT CGTGGCGAT CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 1620  
 TGTGGCGAT CGTGGCGAT CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 1680  
 CGTGGCGAT CGTGGCGAT CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 1740  
 CGGCTCTG ATTTGCTTC AGCGGAGAA CGTACGCGT CGGAGAGTC CGGACGCGCG 1800  
 CGAGCTGAA CGAGGAGTC TGTGGCGAT CGTGGCGCG AGCGATGAAA CGTGGCGCG 1860  
 CGGCGCGCG CGTGGCGAT CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 1920  
 CGGGCGCG CGGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 1980  
 TGTGGCGCG CGGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2040  
 CGGCGCGCG CGTGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2100  
 CGGGCGCG CGGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2160  
 CGGGCGCG CGGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2220  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2280  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2340  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2400  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2460  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2520  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2580  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2640  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2700  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2760  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2820  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2880  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 2940  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 3000  
 CGGCGCGCG CGGCGCG CGGCTCTG CGAGGCGAT CGGACGTTA CGTACGCGCG 3060

AAACGTTTCC	CTTGACGCTCA	ACGGGGTTC	TGGAGGCCG	TGTATTACG	AAGTCGAGTT	3120
CAGCGTTCCG	AATTAAGGCGGA	ACGCGGAGT	CTGAGCGGGC	CTAATCCTCT	CGCCCGCGGC	3180
GAACGCGACG	GACGCCCGGC	CCCGTCAGCG	CTGTTTGTG	GTATGGCTG	GGACGCGCGA	3240
CAACCGGTTG	GACGAGGCGT	CGGCGAAGG	ATGGCCGGA	TGATTTGGGC	CTTTGGTGGC	3300
CGCGCGCGCG	CGCGCGCGCG	GGGAAGTCCC	TCTTACCCCC	ACGACACCGA	CGCCCGCGCG	3360
GGCGTTACCG	GGTTGAGATA	TCTTGAGATA	TCGATCACAC	TGCGCGCGC	TGGAGACCCA	3420
CCACCAUCAC	CACTGAGHTC	CGGCTCTAA	CAAAGCGCGA	AAGGAACTTG	AGTTGGTTTG	3480
TCGGCGCGCT	GAGCAATAAC	TAGCTTAACC	CTTGTGGGCC	TCTAAACGGG	TCTTGCGGCG	3540
TTTTTTGCTG	AAAGGAGGAA	CTATATCCGG	AT			3572

(2) INFORMATION FOR SBC ID NO: 343:

### (b) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## **III. MOLECULAR TYPE: peptides**

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143.

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa  
 1                    5                    10                    15  
 Asp Gly Xaa Arg                    20

(2) INFORMATION FOR SDO TO NSO

#### REFERENCES AND NOTES

- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### MOLECULE TYPE: peptide

(Ex-3) SECURITY DESCRIPTION: SEC IN 202-344.

The Thr Val Pro Xaa Val Thr Glu Ala Arg  
1 2 3 4 5 6 7 8 9

### (2) INTEGRATION OF SEO TO WORKS

(1) ~~SECRET//COMINT//NOFORN~~

- (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TECHNOLOGY: library

#### **MOLEURS TYPE: carpiide**

(x4) SEQUENCE DESCRIPTION: SEQ ID NO: 345.

The Tex Pro Ser Yea Vol 11 No 12 1990

1                    5                    10

## (2) INFORMATION FOR SEQ ID NO:346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp	Ala	Gly	Lys	Xaa	Ala	Gly	Xaa	Asp	Val	Xaa	Arg
1											
											10

## (2) INFORMATION FOR SEQ ID NO:347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr	Xaa	Glu	Glu	Xaa	Gln	Glu	Ser	Phe	Asn	Ser	Ala	Ala	Pro	Gly	Asn
1															16
															Xaa Lys

## (2) INFORMATION FOR SEQ ID NO:348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTACTTGTATA CTGCACTCGCA GACCGTCG

27

## (2) INFORMATION FOR SEQ ID NO:349:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTGACCA ATTCACTTCC ACTCCT

28

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCC ATCATCATCA TCATCACGTC ATCGACATCA TCGGGACCG CGCGACATCC	60
TGTTAACAGG CGGGCTTGA GGTTGTCGGG CGGGCGCGG ATACCTTGA TGACATCCCG	120
GTCGCTGGG TCATGACCA GAGATGCGG CTGGACAGCG CGGGCAASAT CACCTACCGC	180
ATCAAGCTCG AAGTGTGTT AAAGATGAGG CGGGCGAAC CGAGGGGTC GAACGACCC	240
AGCGTTGCG CTGAAACCG CGGGCGCGC AGCTTGTGCG CAACTACCC CGCTCGCTCG	300
CGCTTACGT TGGCGAGG CGTACGACG CGCTCTTACG CGCTGTTCAA CGTGTGCGT	360
CGCTCTTTC AGGAGAGTA TCGAACGTC AGCTTACCG CGGGCGCGC CGCTTCTGGT	420
CGGGCGCGT CGCGCTCG CGGGGGGCG CGTACACATTG CGGCTCGGA CGCTTCTCG	480
TCCGAGGTC ATATGCTTC GCACAAGGG CGTGTGAAACA TCGCGCTAGC CGTGTCCGT	540
CGGGAGCTCA ACTRACACT CGGGGGGTC AGCGACACC CGTACGTTCA CGGAAAAGTC	600
CTGGCGCGCA TGTACGCGG CGCTCTCAA ACTTGTGACG ACCGGCGAT CGCTTGCGTC	660
AACTGGGGG TGAACTTCG CGGGCGCG CGTACGTTCGC TCGACGCGT CGACGGGTG	720
CGTACACGT TGTCTTTCG CGGGCGCG CGGGCGCG CGTACGAAAG ATATGCTTC CGGGCGCG	780
TGGGGCGGT TGGACGCG CGTACGTTTCG CGGGCGCG CGTACGAAAC	840
CGGAAACGGG CGCTGGTAC CGGGCGCG CGGGCGCG CGTACGACCG CGTACGATGC	900
ATCGACGTTTC TGTACGAGGC CGTACGACCG CGGGCGCG AGGGCGACT AGGCAATRG	960
TGTGGGATT TGTCTTTCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1020
CGGGAAACCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1080
CGGATGTCG ACTRACACTA CGGGCGCG AACGACGGGC AAAAGGACCC CGGGCGCG	1140
CGGGCGCG AGGGCGTT CGGGCGCG CGTACGACCG CGGGCGCG CGGGCGCG	1200
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1260
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1320
AATTCGCGAC CGATCTCGCG CGGGCGCG AACGGCGAT CGGGCGCG CGGGCGCG	1380
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1440
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1500
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1560
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1620
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1680
CGGGCGCG AGGGCGTT CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1740
ATTCGCGCG AGGGCGCG AGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1800
CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1860
CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1920
CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	1980
CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	2040
ACGGCGATCA AGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	2100
TATTCGCGAC CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG CGGGCGCG	2160

ATGCGTTTCG CCGCCCGGAA CGCGCGGAC CGCGGGCGGC CTTCAGCGCTG GTTTCGGATA	2220
TGGCTGGAA CGCGCGAACG CGCGGTGGAC AAGGGCGCGG CGAGGGCGT CGCGCGATCG	2260
ATCGCGCTTT TGGCGCGCGC CGCGCGCGC CGCGCGCGG CGCGCGCGA CGCGCGCGC	2340
CGCGCGCGGCG CGCGCGCGGA AGTCGCGCT ACCCGCGAAC CGACCGACG CGCGCGACC	2400
TTTACCGCTT GA	2412

## (i) INFORMATION FOR SEQ ID NO:351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser  
 1 5 10 15  
 Pro Thr Ser Trp Glu Gln Ala Ala Glu Ala Val Gln Arg Ala Arg  
 20 25 30  
 Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met  
 35 40 45  
 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val  
 50 55 60  
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser  
 65 70 75 80  
 Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro  
 85 90 95  
 Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr  
 100 105 110  
 Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn  
 115 120 125  
 Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Glu  
 130 135 140  
 Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser  
 145 150 155 160  
 Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala  
 165 170 175  
 Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His  
 180 185 190  
 Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile  
 195 200 205  
 Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn  
 210 215 220  
 Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly  
 225 230 235 240  
 Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly  
 245 250 255  
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val  
 260 265 270  
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys  
 275 280 285  
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp

290	295	300
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser		
305	310	315
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala		
320		
325	330	335
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp		
340	345	350
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile		
355	360	365
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala		
370	375	380
Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp		
385	390	395
Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp		
400		
405	410	415
Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala		
420	425	430
Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu		
435	440	445
Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly		
450	455	460
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg		
465	470	475
Phe Gln Glu Ala Ala Asn Lys Gln Lys Glu Leu Asp Glu Ile Ser		
480	485	490
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu		
500	505	510
Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala		
515	520	525
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro		
530	535	540
Val Ala Pro Pro Pro Ala Ala Asn Thr Pro Asn Ala Gln Pro		
545	550	555
Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro		
565	570	575
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn		
585	590	595
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser		
595	600	605
Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr		
610	615	620
Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr		
625	630	635
Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu		
645	650	655
Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu		
660	665	670
Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser		
675	680	685
Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys		
690	695	700
Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile		
705	710	715
Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp		
720	725	730

Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala  
 740 745 750  
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro  
 755 760 765  
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala  
 770 775 780  
 Gly Glu Val Ala Pro Thr Pro Thr Pro Thr Pro Gln Arg Thr Leu  
 785 790 795 800  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO:352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CAGTCAGCGG TTCCGCGTCAA ACCG

34

## (2) INFORMATION FOR SEQ ID NO:353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CCCTTCAAAAT TCACCTTGCGG AGGAAATCGT CCGCGATC

37

## (2) INFORMATION FOR SEQ ID NO:354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

CGATGTGCC ATGATGAAAGA TCATCACCGGA TCCAAACCAC CGACGCGTTG GCCTGAAAGG	60
CGCGCGCG CGCGTACTGT CGCGGACTAACG CGCGCGTGTG CGCGCGTACG GTTGGCGGAG	120
ACCGGGTAGCA CGCTCTTTTA CGCGCTTTC AACCTTTGGG CGCGCGTTT TCACGAAAGG	180
TATCCGAAAGG TCGCGATGAC CGCTCAAGGC AGCTTTTGTG CGCGGGGGT CGCGCGAGGC	240

CCCGGGGGA CGCTGAGCT TGGGGCTCC GACGCTATC TGTCGGAAAG TGATATGCC	300
CCGCACAGG CGCTGATGAA CATCGCCTTA CGCTCTTGG CTCTGGAGT CAACTAAC	360
CTGGCGCGAG TGAGCTGAGCA CCTCAAGCTG AAGCGAAGTG TCTGGCGGC CATCTACCG	420
GCGACCGCTCA AAACCTGGGA CGACCGCGAG ATCTGCTGTC TCAACCCCGG CGTGCACCTG	480
CCCGCGACCG CGGTAGTTCC GTGCGACCGC TCGAGCTGCT CGTCTGCGCT TTGTTTTTC	540
ACCCAGTACG TGTGCGAGCA AGTGTGGAG CGCTGGGCA ACTGCGCCCG CTGGCGAC	600
ACCGTGTAGT TCCCGGGCTG CGCGGGTGGCG CTGGGTGAGA ACGGCAACGG CGCGATGGT	660
ACCGGGTTGG CGAGAGACACG CGCTCTGGTG GCCTATATCG GCGTACGCTT CCTCGACCG	720
CCCACTGAAAC GCGGACTCG CGAGGCCAA CTAGCGCTAA GCTCTGGCRA TTTCCTTTTG	780
CCCGACGCGC AAAGCGATTCA CGCGCGCGCG CGCTGGCTTC CGTGCAGAAC CGCGACGAC	840
CGGGCGATT CGATGATGCA CGCGCTCGC CGCGACGCT ACCCGATCAT CGACTACAG	900
TACGGATGG TCAACAAACG CGAGAGACG CGCGCGCGCG CGCAGACCTT CGCGACGTT	960
CTGCACTGGG CGATCGCCG CGGCGACAG CGCTGGTCC TCGAGCTGCT TCATTTCCAG	1020
CGCTGGCG CGCGCGTTG CTGCTGGT GACGCTTGA TGGGAGCAT TTGTCGCGA	1080
GATGCGATG CGCGGGCTC AGCTGAGCT TCTGGCGGAA CGCTGGCGAC AACGCGCGGC	1140
TGCGCGCGT CGATGCTGC ACCGGCACCT CGACGGCGCA CGCTGGTTCG CGCGCGACCA	1200
CGCGCGCGCG CGAACCGCCG GAAGGCCAG CGCGCGCGCG CGAACCGCAGC ACCTGGCGCG	1260
CGAGCGCG CGCGACCGCC CGCGCGCGT ATTGGCGCA ACCGGCGCA ACCTGGCGCG	1320
ATCGACAAACG CGGTTGGAGG ATTGGCTTTC CGCGCTCGT CGCTGGCTGT CGAGCTCTGAC	1380
CGCGCGCGCT TCGACTACGG TTCTGGCGTC CTGAGCGAA CGAGCGCGGA CGCGCGATTT	1440
CTGAGACGCG CGCGCGCGT CGCGCGCGAC ACCGGTATCG CGCTGGCGCG CGTACGCGA	1500
AAGCTTACG CGACGGCGCA AGCGACCGAC CGCAAGGGCG CGCGCGCGT CGCTGGAC	1560
ATGAGTGAATCT TCTATATGCC CTACGGCGCG ACCGGATCG ACCGGAAAC CGCTGGCGTC	1620
GAAGGGCGACG CGCTGGCTTG AAGCGCGCTG TATTCGAGAG TCAAGTTTCAG CGATCGCGT	1680
AAGCTTACG CGCGATCTG CGAGCGCGCA ATCGCGCTCG CGCGCGCGAC CGCGCGCGAC	1740
CGCGCGCGCG CGCGCGCGCG CGTCTGGTGA TGGCTGGCGA CGCGCGCGAA CGCGCGCGAC	1800
AAGCGCGCG CGCGCGCGT CGCGCGCGCG ATCGCGCGCGT CGCTGGCGCG CGCGCGCGCG	1860
CGCGCGCGCG CGCTGGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG CGCGCGCGCG	1920
ACCGCGACCG CGCGACGACG CGAGCGCGACG TTACCGGGCT GR	1980

## (2) INFORMATION FOR SEQ ID NO:355:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Gly His His His His His His Gly Ser Lys Pro Pro Ser Gly Ser			
1	5	10	15
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser			
16	20	25	30
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu			
35	40	45	
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr			
50	55	60	
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala			
65	70	75	80
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly			
85	90	95	
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser			

105	105	110
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys		
115	120	125
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr		
130	135	140
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro		
145	150	155
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr		
165	170	175
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly		
180	185	190
Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly		
195	200	205
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu		
210	215	220
Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala		
225	230	235
Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn		
245	250	255
Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe		
260	265	270
Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro		
275	280	285
Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn		
290	295	300
Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu		
305	310	315
His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val		
320	325	330
His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu		
340	345	350
Ile Ala Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly		
355	360	365
Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr		
370	375	380
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro		
385	390	395
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala		
405	410	415
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro		
420	425	430
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser		
435	440	445
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp		
450	455	460
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro		
465	470	475
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg		
485	490	495
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala		
500	505	510
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro		
515	520	525
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val		
530	535	540

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Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys  
545 550 555 560  
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn  
565 570 575  
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly  
580 585 590  
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu  
595 600 605  
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro  
610 615 620  
Ala Glu Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr  
625 630 635 640  
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala  
645 650

## CLAIMS

1. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gin-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128) and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative

substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

3. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341 or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. An expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.
8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A pharmaceutical composition comprising one or more polypeptides according to any one of claims 1-4 and a physiologically acceptable carrier.
10. A pharmaceutical composition comprising one or more DNA molecules according to claim 5 and a physiologically acceptable carrier.
11. A pharmaceutical composition comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a physiologically acceptable carrier.
12. A vaccine comprising one or more polypeptides according to any one of claims 1-4 and a non-specific immune response enhancer.
13. A vaccine comprising:
  - a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
  - a non-specific immune response enhancer.
14. A vaccine comprising:
  - one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

a non-specific immune response enhancer.

15. The vaccine of claims 12-14 wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine comprising one or more DNA molecules according to claim 5 and a non-specific immune response enhancer.

17. A vaccine comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a non-specific immune response enhancer.

18. The vaccine of claims 16 or 17 wherein the non-specific immune response enhancer is an adjuvant.

19. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 9-11.

20. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 12-18.

21. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

22. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6.

23. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO:155).

24. A pharmaceutical composition comprising a fusion protein according to any one of claims 21-23 and a physiologically acceptable carrier.

25. A vaccine comprising a fusion protein according to any one of claims 21-23 and a non-specific immune response enhancer.

26. The vaccine of claim 25 wherein the non-specific immune response enhancer is an adjuvant.

27. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 24.

28. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to claims 25 or 26.

29. A method for detecting tuberculosis in a patient, comprising:  
(a) contacting dermal cells of a patient with one or more polypeptides according to any one of claims 1-4; and  
(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

30. A method for detecting tuberculosis in a patient, comprising:  
(a) contacting dermal cells of a patient with a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and  
(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

31. A method for detecting tuberculosis in a patient, comprising:  
(a) contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308,

310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

32. The method of any one of claims 29-31 wherein the immune response is induration.

33. A diagnostic kit comprising:  
(a) a polypeptide according to any one of claims 1-4; and  
(b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

34. A diagnostic kit comprising:  
(a) a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and  
(b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

35. A diagnostic kit comprising:  
(a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and  
(b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

36. A diagnostic kit comprising:

- (a) a fusion protein according to any one of claims 21-23; and
- (b) apparatus sufficient to contact said fusion protein with the dermal cells of a patient.

37. A fusion protein according to claim 23 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 153, 209, 351 and 355.

## D7 T Cell Proliferation

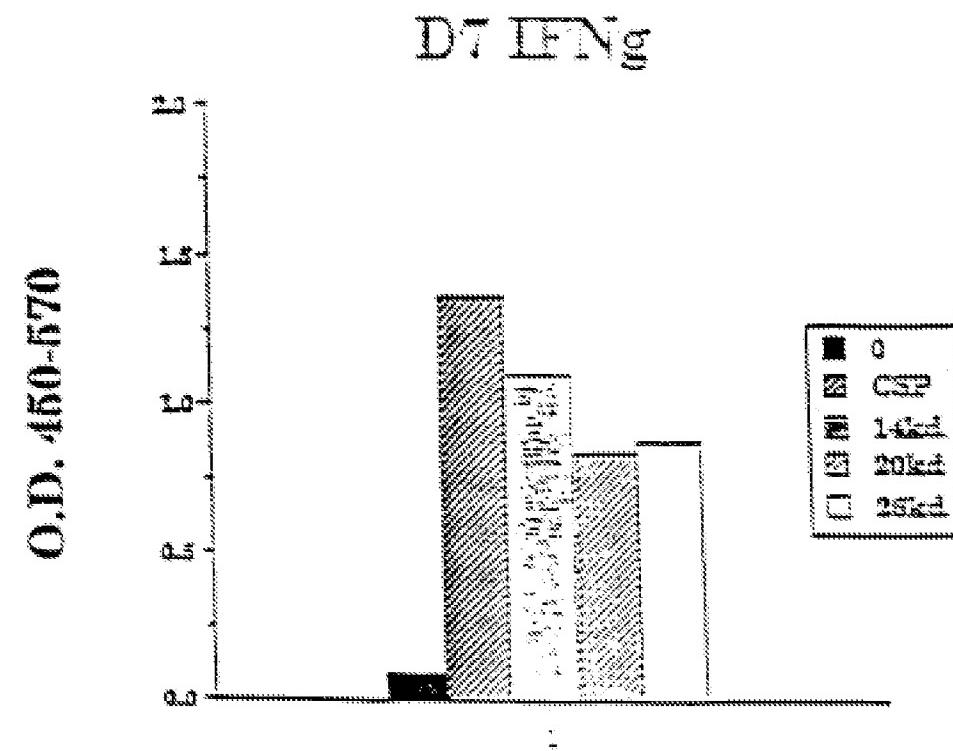
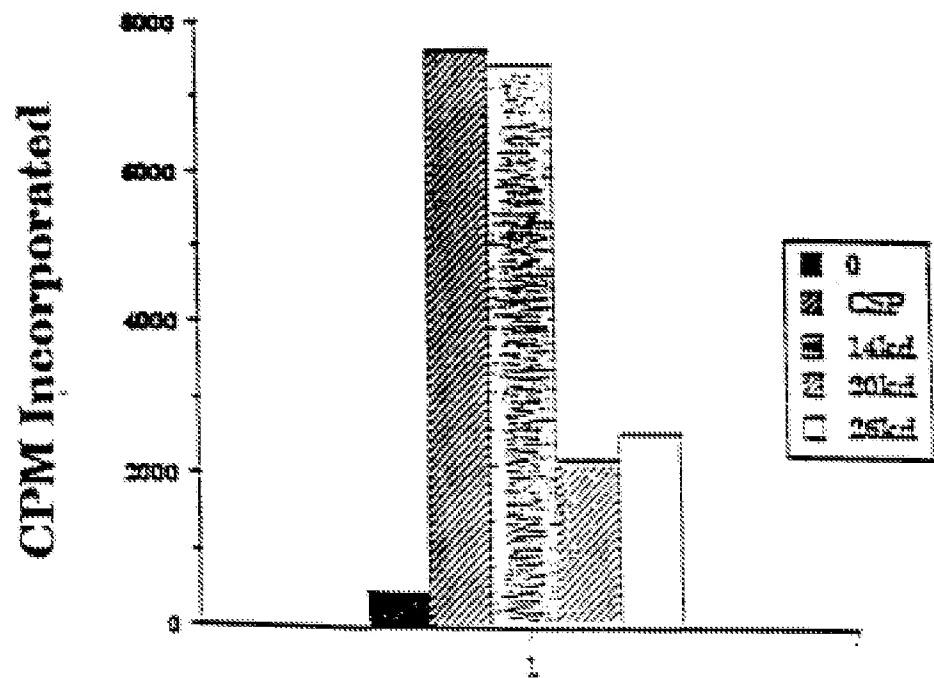
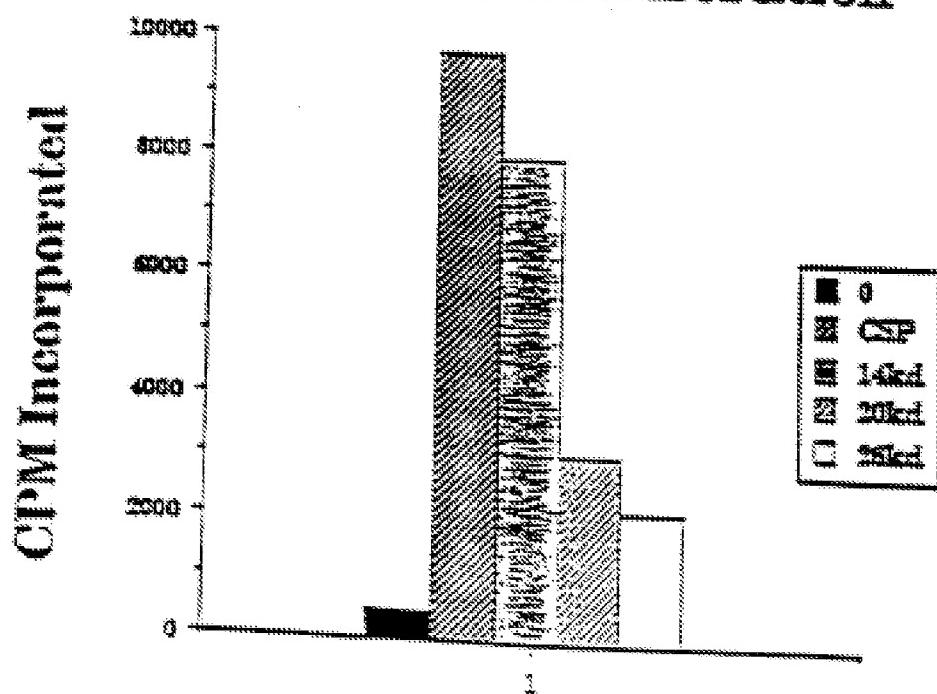


FIG. 14

### D160 T Cell Proliferation



### D160 IFNg

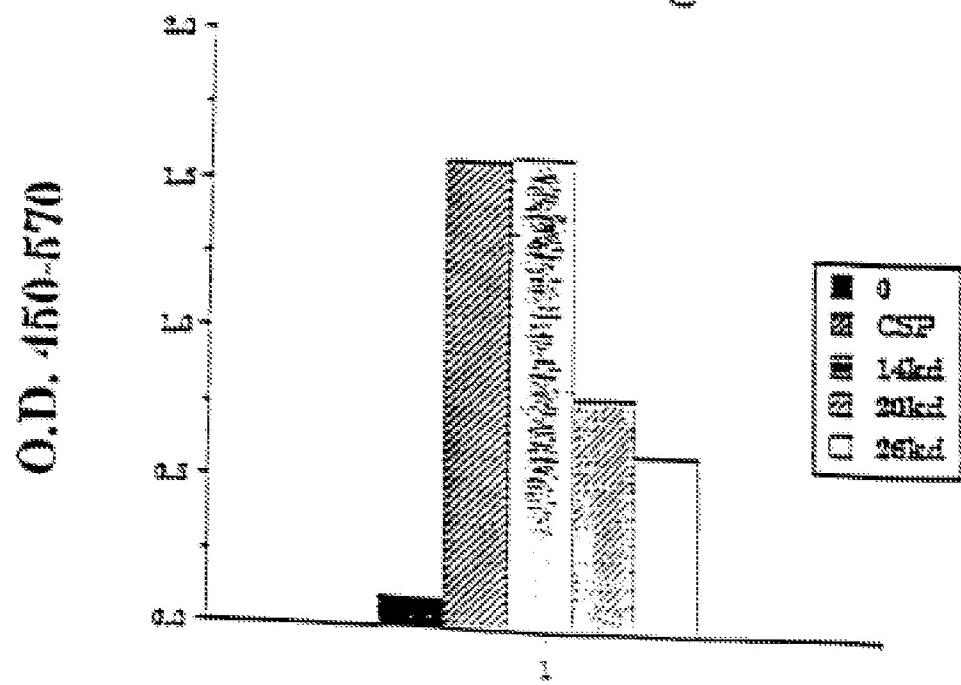


FIG. 1B

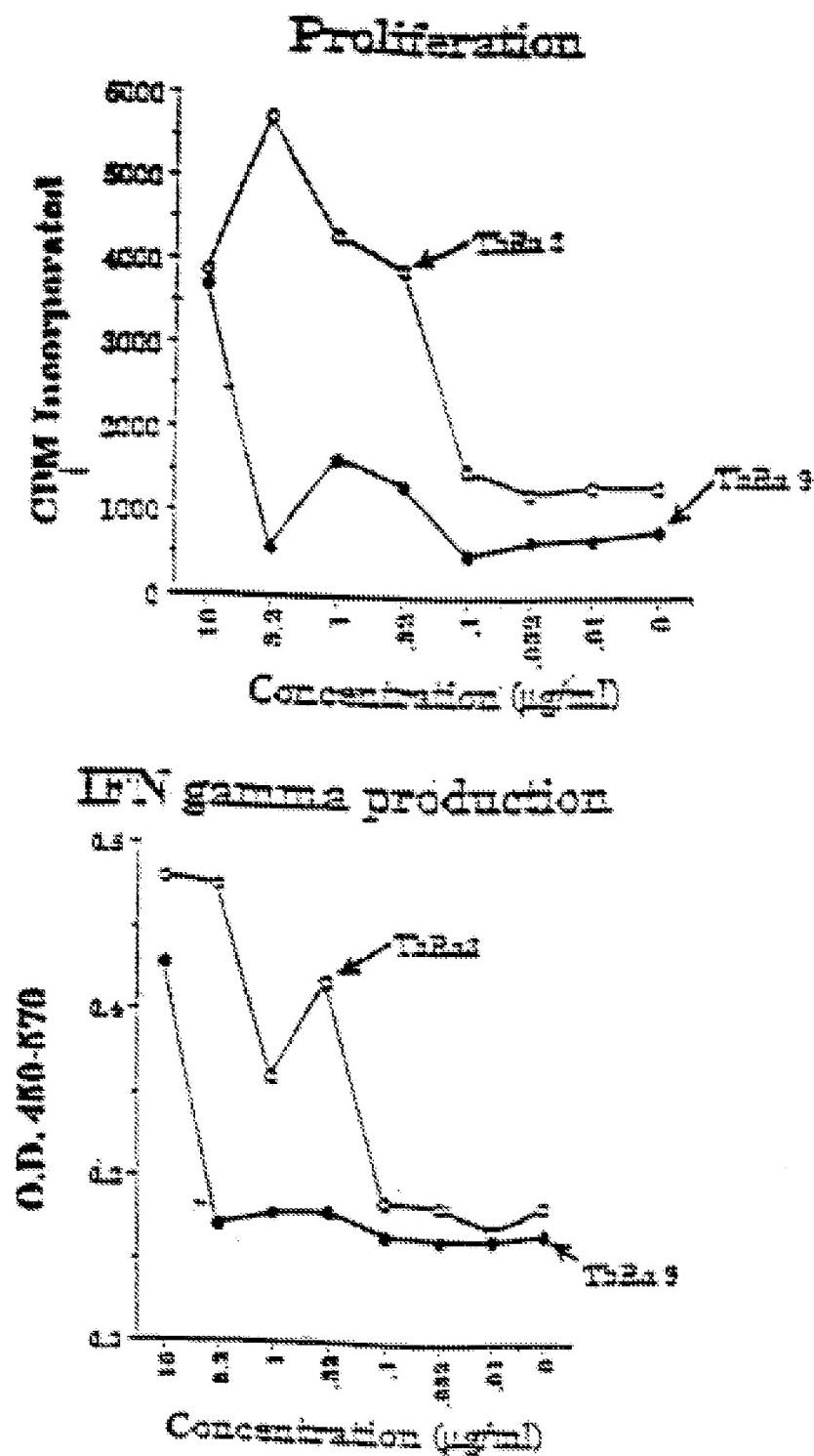
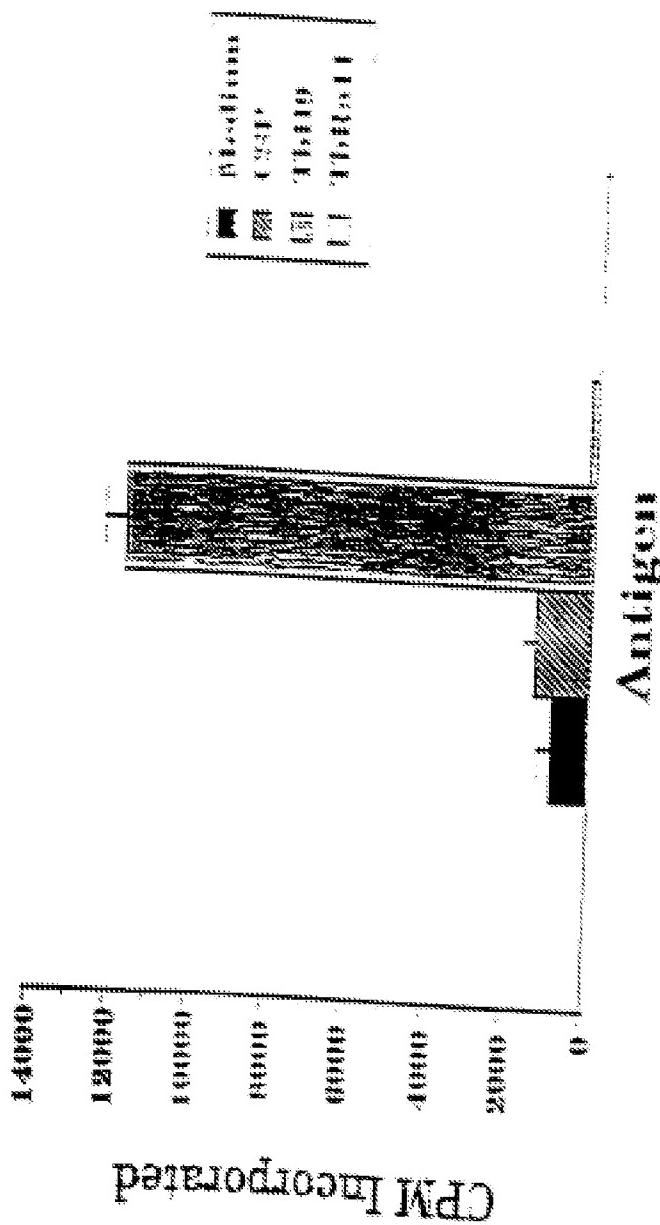


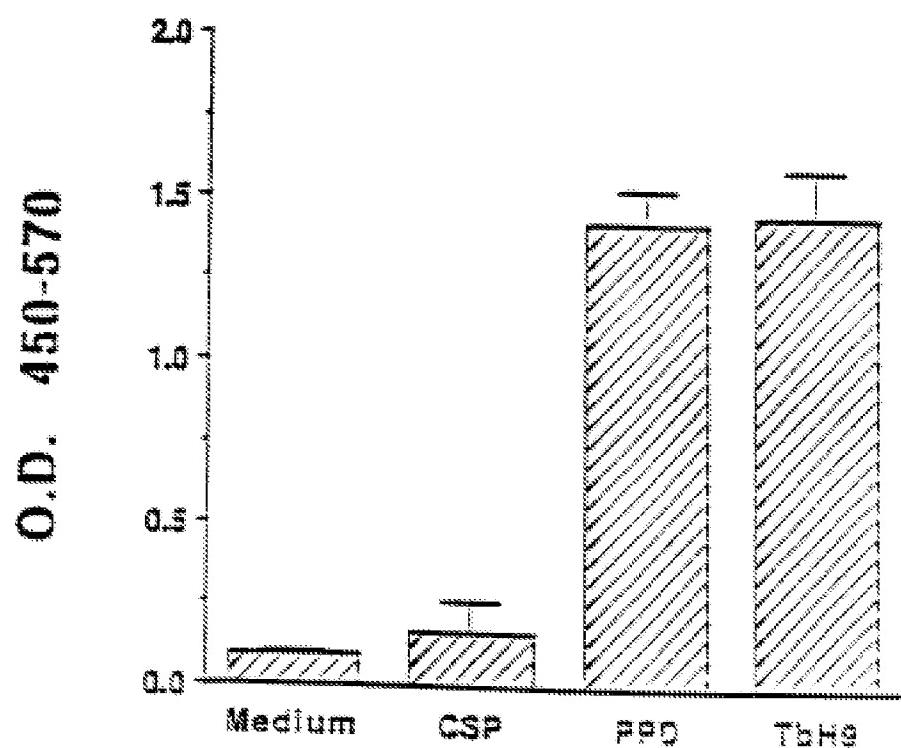
FIG. 2



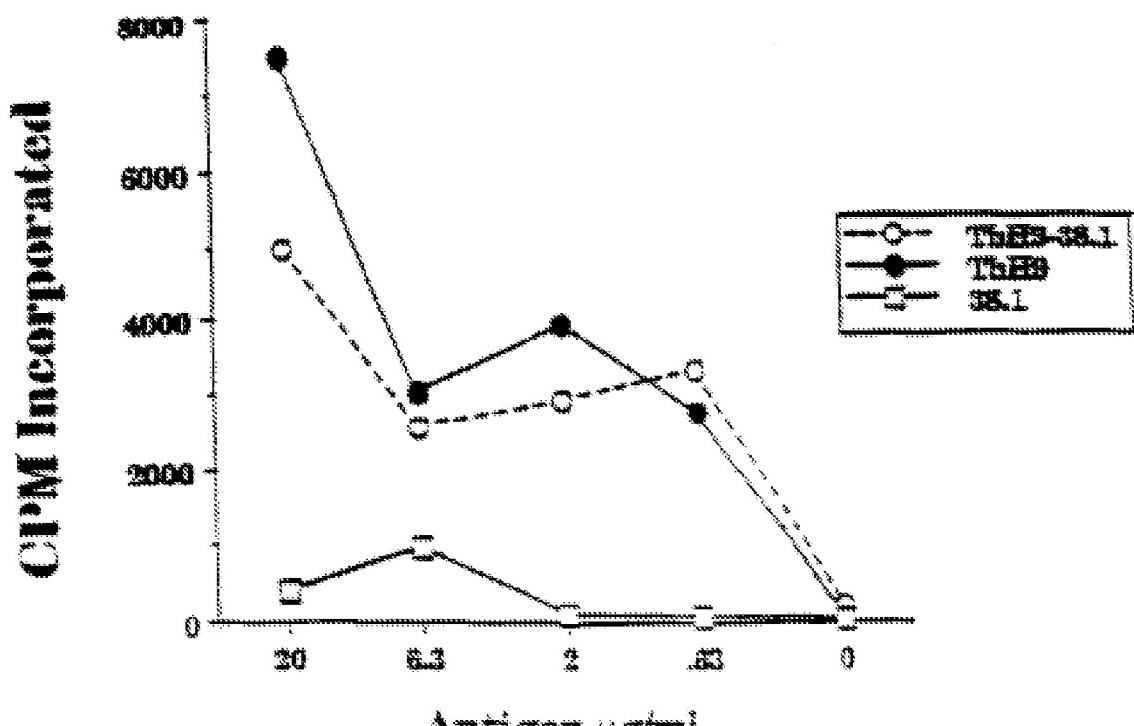
T cell clone 131Tb/H9 responds poorly to CSF



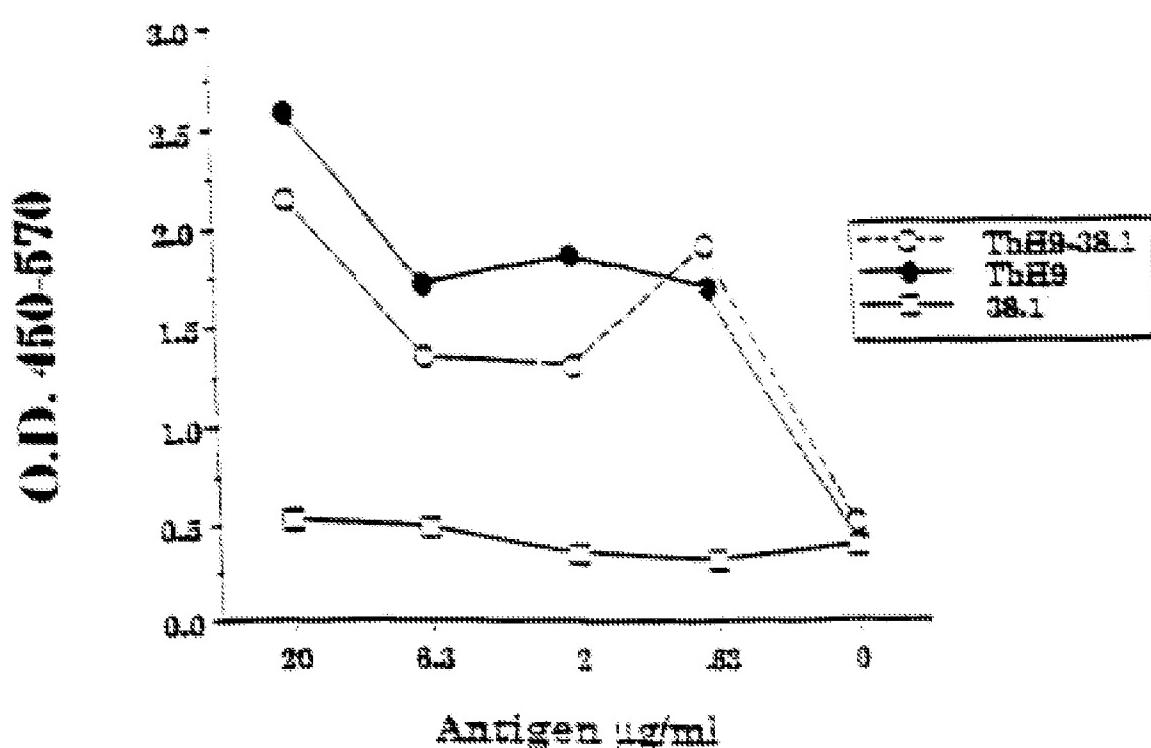
三

**T Cell Clone PPD 800-10 IFNg Production***FIG. 4B*

## D131 T Cell Proliferation

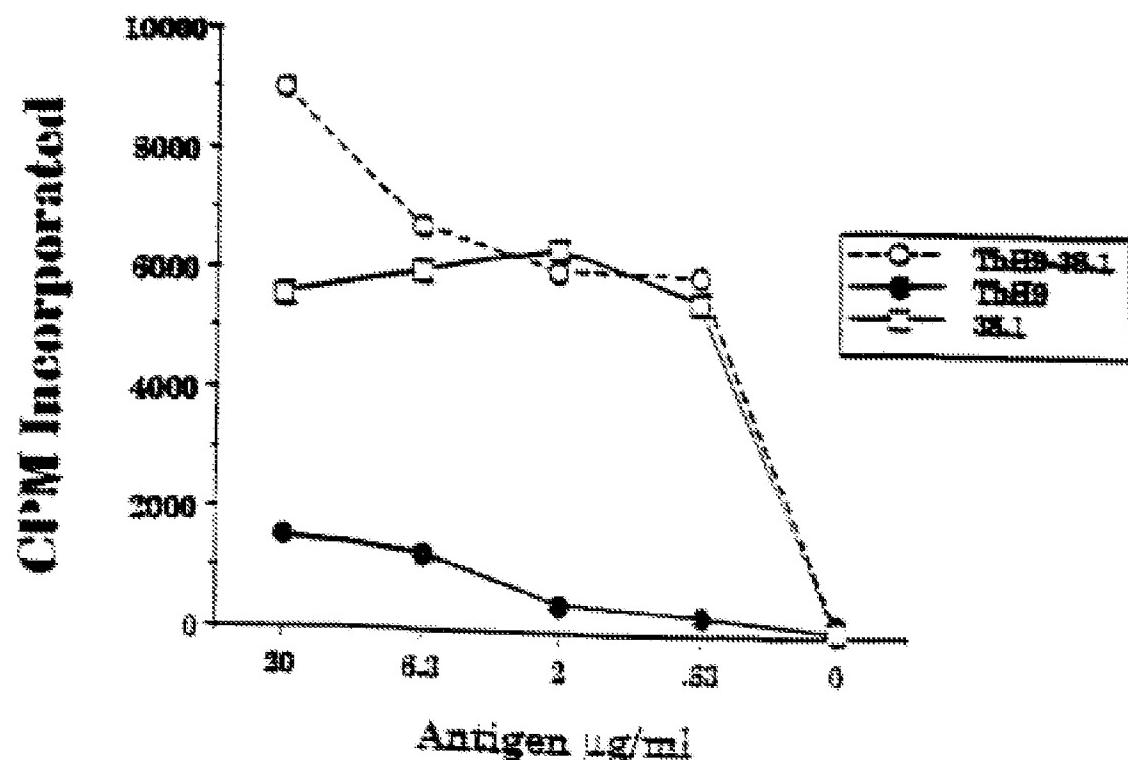


## D131 IFNg

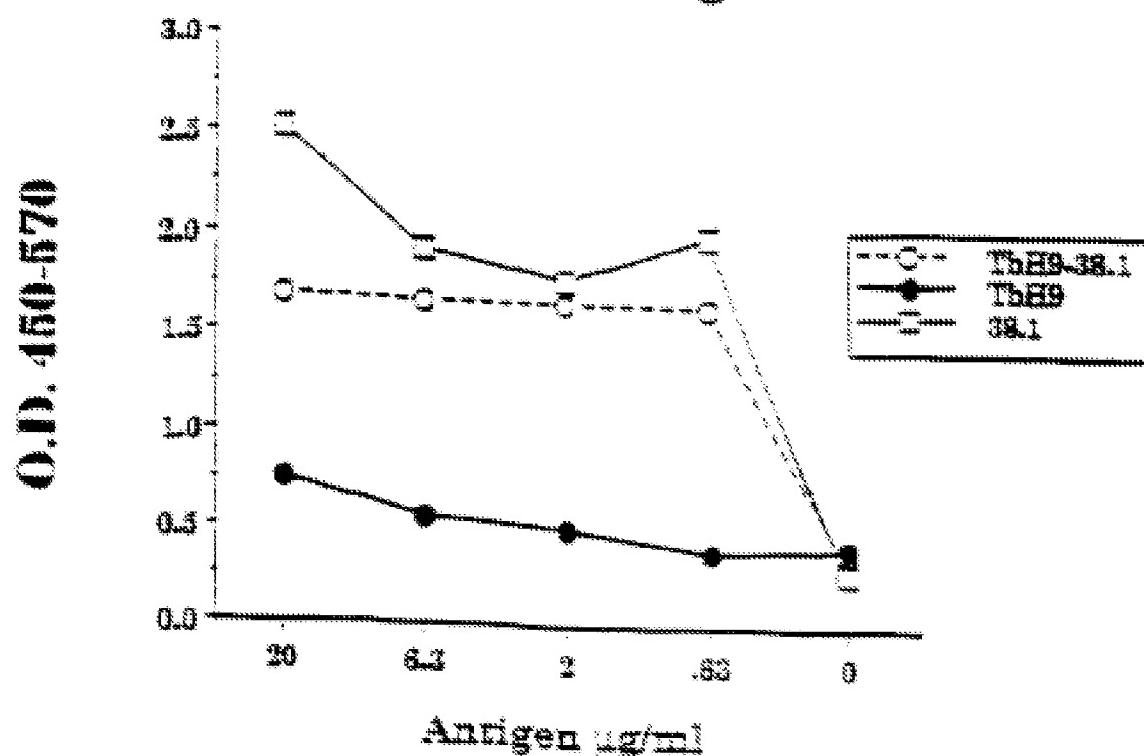


FIGS. 5.A-B

## D184 T Cell Proliferation

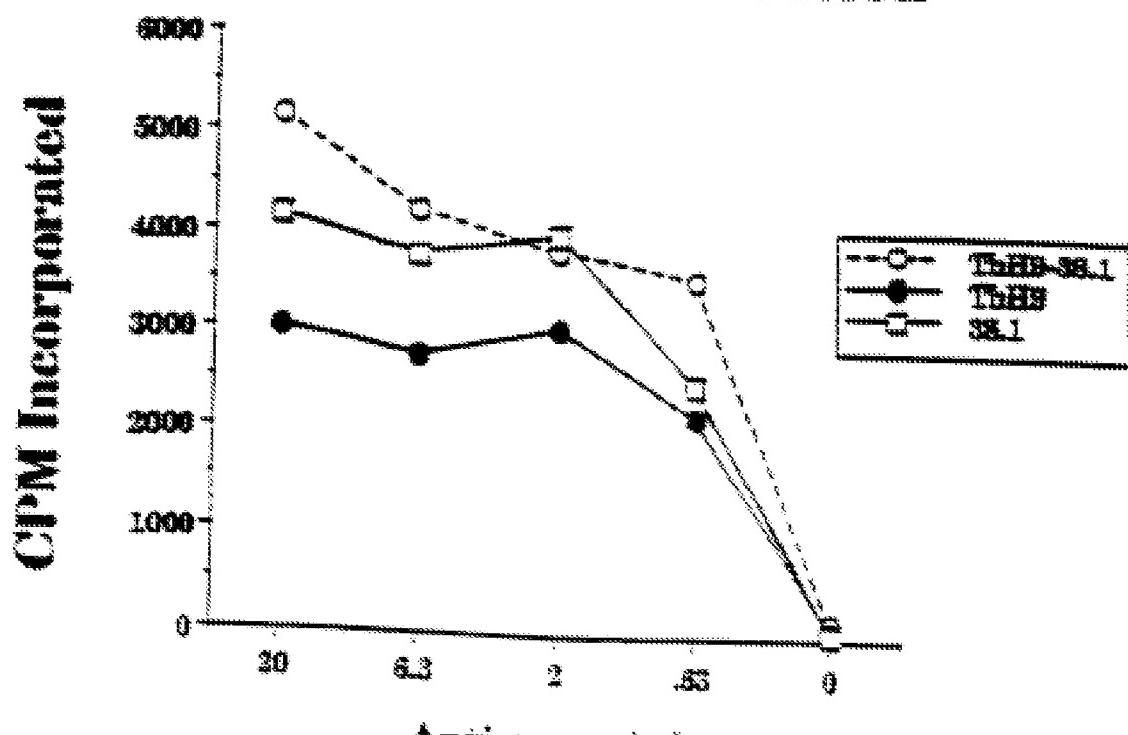


## D184 IFNg

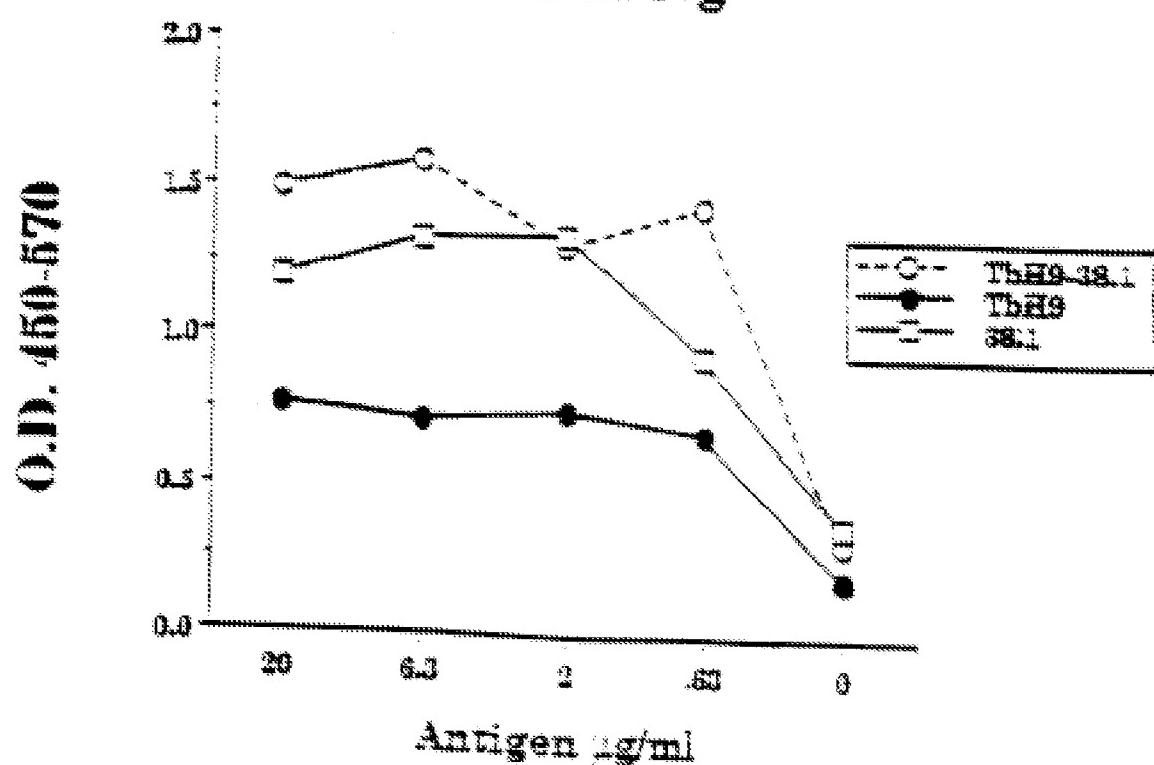


FIGS. 6 A-B

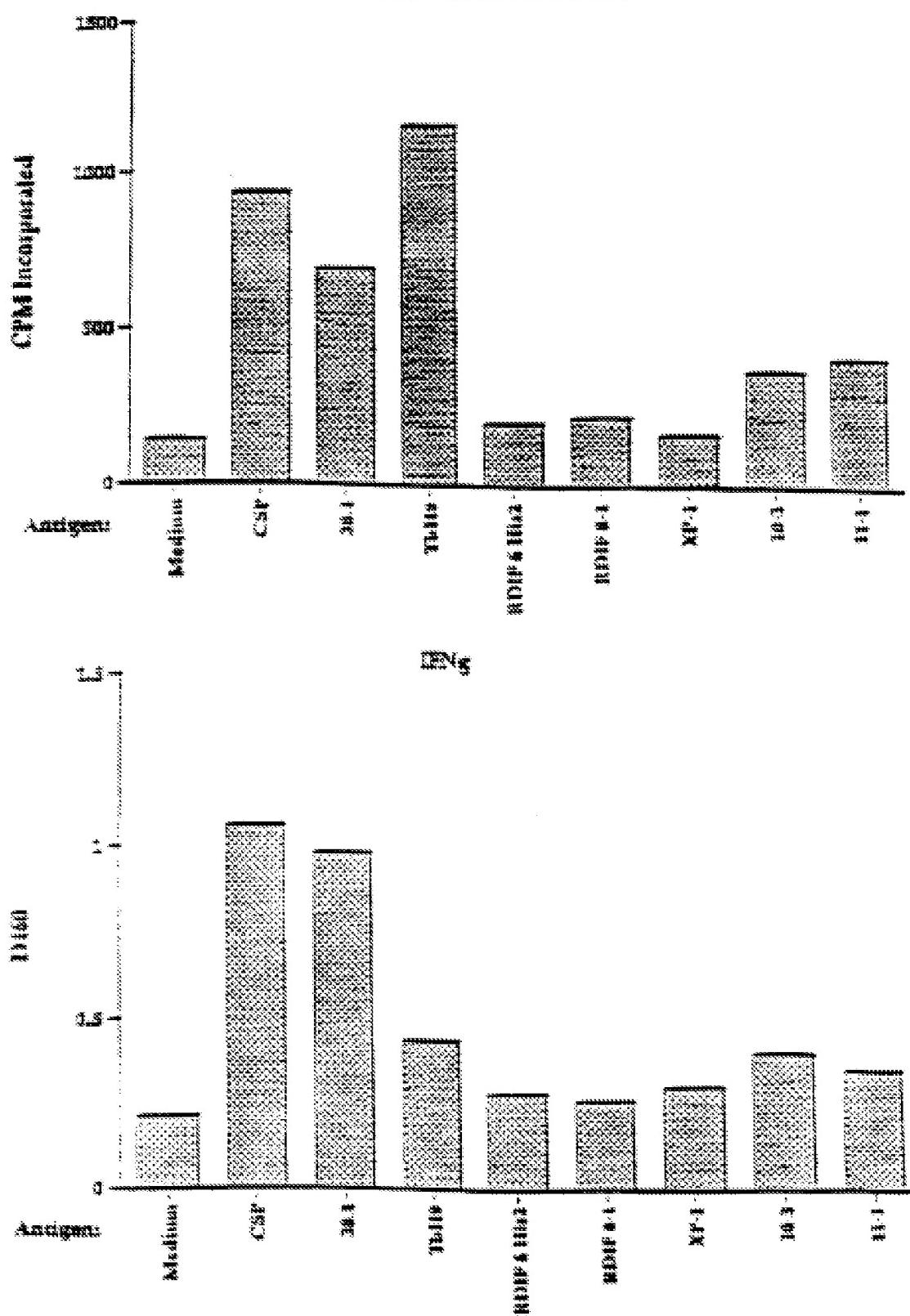
### D201 T Cell Proliferation

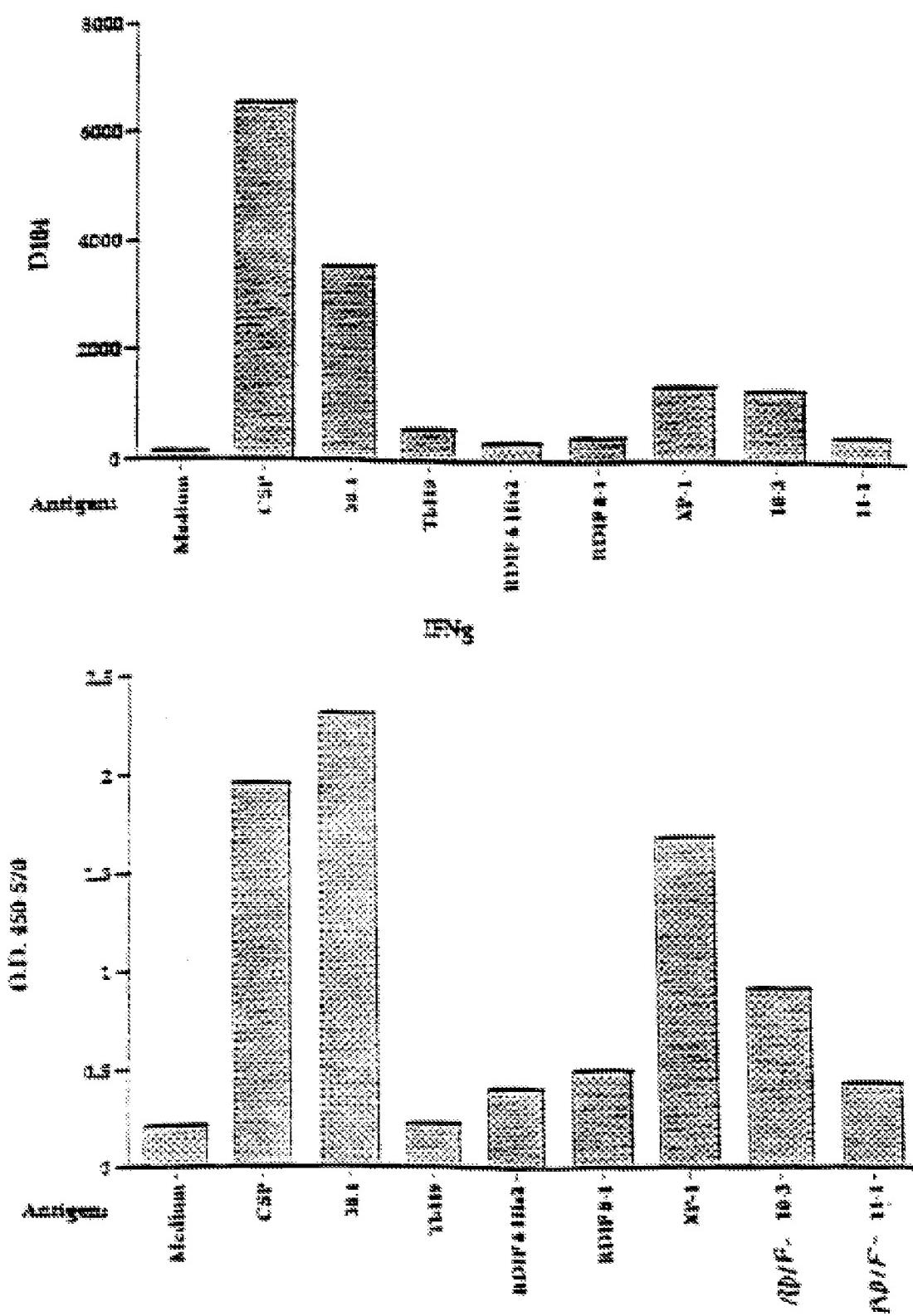


### D201 IFNg

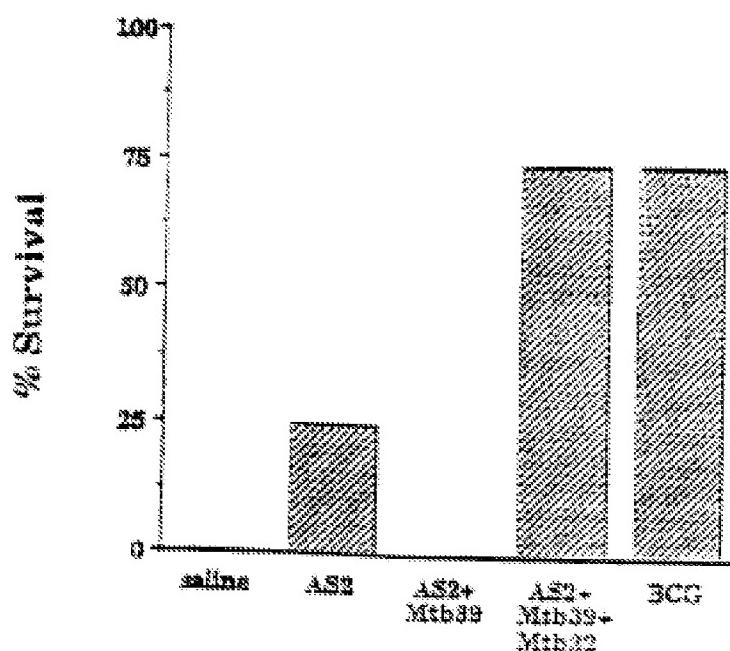


FIGS. 7A-B

**Dose T Cell Proliferation****FIGS. 8A-B**

**DIMA T Cell Proliferation****FIGS. 9A-B**

**Tuberculosis: Protection of Cynomolgus Monkeys  
with Recombinant Antigens of Mtb**



**FIG. 10**

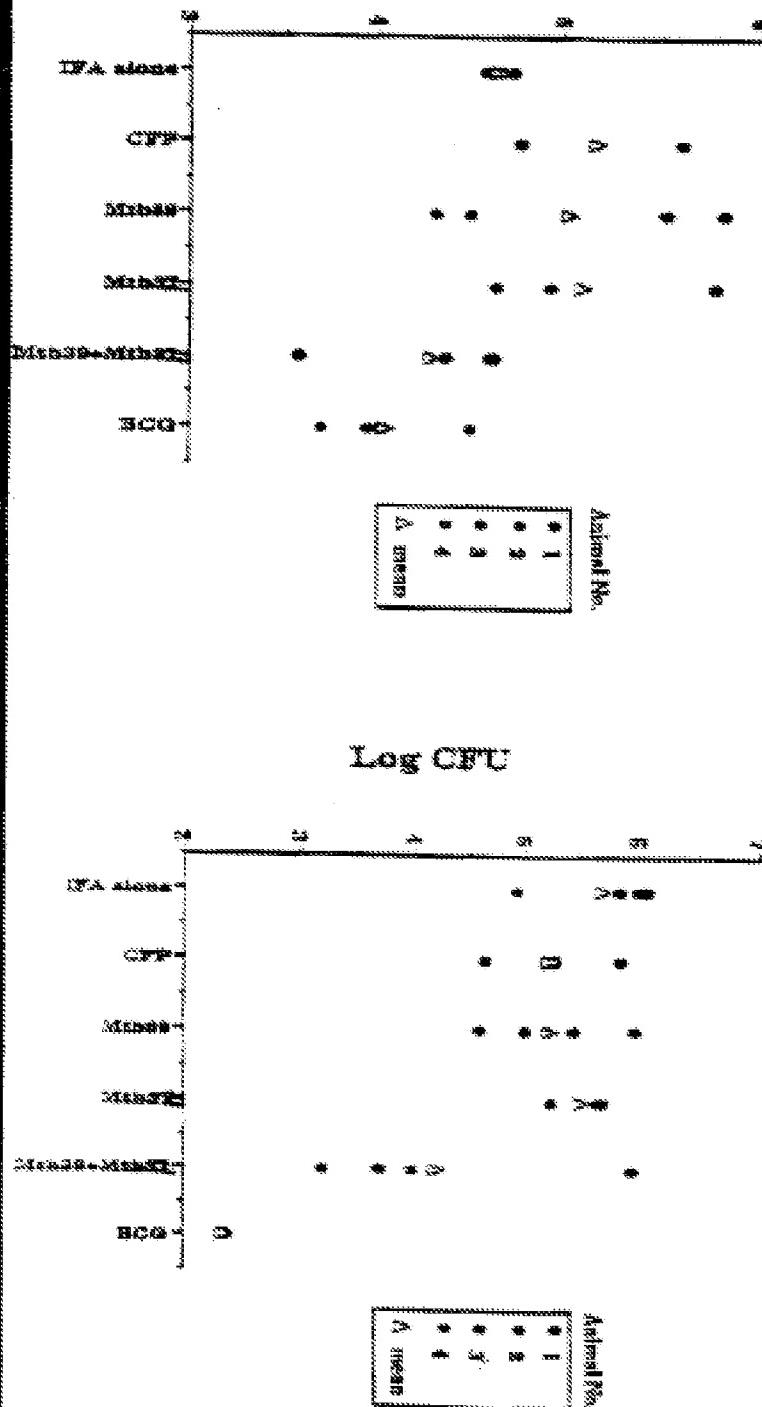
# Aeromethyl TB Challenge of Vaccinated and Unvaccinated Pigs

Lung CFU

Spleen CFU

Log CFU

Log CFU



FIGS. 11 A-B

## DNA Immunized mice challenged with aerosol TB (lung CFU)

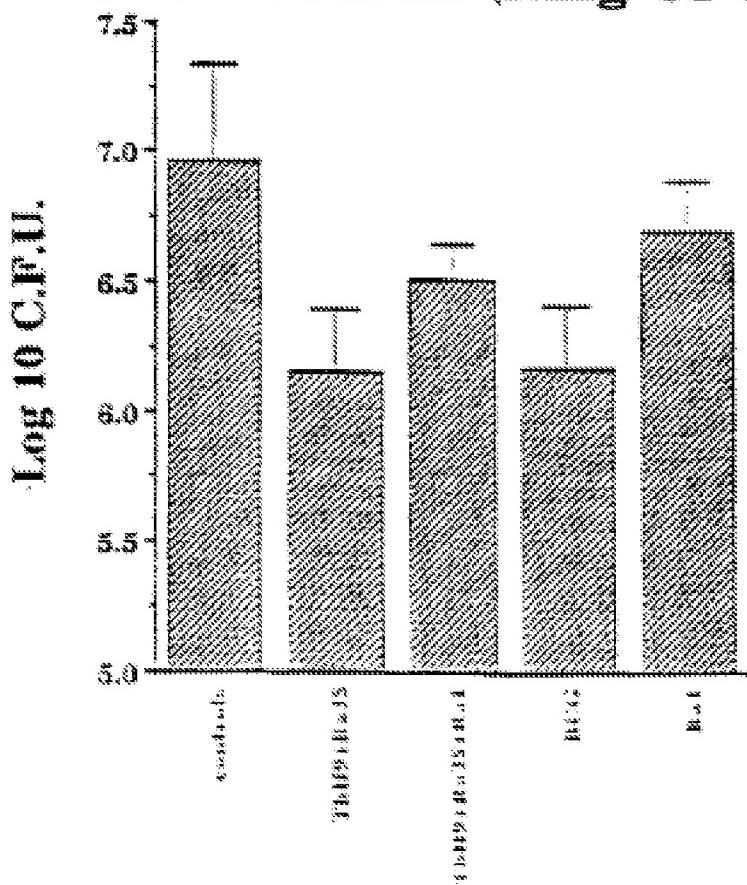


FIG. 12